



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 167420

TO: Lorraine Spector  
Location: 4d55 / 4c70  
Monday, October 03, 2005  
Art Unit: 1647  
Phone: 571-272-0893  
Serial Number: 09 / 674377

From: Jan Delaval  
Location: Biotech-Chem Library  
Remsen 1a51  
Phone: 571-272-2504

jan.delaval@uspto.gov

### Search Notes

Rest 10/4/05

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167420

STIC-Biotech/ChemLib

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From: Spector, Lorraine  
Sent: Friday, September 30, 2005 1:42 PM  
To: STIC-Biotech/ChemLib  
Subject: SEARCH request for Serial No. 09/674377

STIC,

Please search SEQ ID NO: 1 and 2

-pending

-issued

-commercial

Also, please align the two sequences with each other.

Thanks.

Lorraine Spector  
571-272-0893  
U.S. Patent and Trademark Office  
Art Unit 1647  
lorraine.spector@uspto.gov  
Office: Remsen 4D-55  
Mailbox: Remsen 4C-70

\*\*\*\*\*

Searcher: Jan  
Searcher Phone: 22504  
Date Searcher Picked up: 10/3/05  
Date completed: 10/3/05  
Searcher Prep Time: 10  
Online Time: 20

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# ✓  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: ✓  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor  
Remsen Bldg. 01 D86  
571-272-2507

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:29 ; Search time 40.225 Seconds  
(without alignments)  
1069.209 Million cell updates/sec

Title: US-09-674-377B-1

Perfect score: 2604  
Sequence: 1 ERKRNTIHEPKSAKTLTI.....IPWDYCPISRCGDTPTIV 447

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2601	99.9	728	1 JH0579	hepatocyte growth
2	2408	92.5	728	1 A60185	hepatocyte growth
3	2401	92.2	728	1 A35644	hepatocyte growth
4	1864.5	71.6	710	1 I51283	hepatocyte growth
5	1737.5	66.7	411	2 I51285	hepatocyte growth
6	1180.5	45.3	711	1 A47136	macrophage-stimula
7	1144	43.9	716	1 JCS061	macrophage-stimula
8	1135	43.2	716	1 A40332	macrophage-stimula
9	1066	40.9	790	1 PLPG	plasma (EC 3.4.21
10	1059	40.7	812	1 PLMS	plasma (EC 3.4.21
11	1053.5	40.5	810	2 I46260	plasma (EC 3.4.21
12	1044.5	40.1	810	2 B30848	plasma (EC 3.4.21
13	1042	40.0	810	1 PLHU	plasma (EC 3.4.21
14	1038	39.9	812	1 PLBO	plasma (EC 3.4.21
15	943.5	36.2	2869	2 T18518	apolipoprotein(a)
16	879	33.8	4548	1 S00657	apolipoprotein(a) (EC
17	843.5	32.4	1420	2 A32869	apolipoprotein(a)
18	457	17.5	460	2 B61545	plasma (EC 3.4.21
19	454	17.4	455	2 A61545	plasma (EC 3.4.21
20	408.5	15.7	336	2 S33879	plasma precursor
21	357.5	13.7	625	1 TBBO	thrombin (EC 3.4.2
22	353	13.6	169	2 A40522	plasma (EC 3.4.21
23	352.5	13.5	618	2 A35827	thrombin (EC 3.4.2
24	350	13.4	622	1 TBHU	thrombin (EC 3.4.2
25	344	13.2	617	2 S10511	thrombin (EC 3.4.2
26	307.5	11.8	559	1 A35029	c-plasminogen acti
27	303	11.6	562	1 UKHUT	c-plasminogen acti
28	297.5	11.4	559	1 A29941	c-plasminogen acti
29	270	10.4	120	2 B61545	plasma (EC 3.4.21

30	268	10.3	123	2 C61545	plasma (EC 3.4.21
31	260.5	10.0	89	2 A60140	plasma (EC 3.4.21
32	235.5	9.0	946	1 A47299	ror-related recep
33	230	8.8	943	2 B45082	neurotrophic recep
34	228.5	8.8	603	2 S28941	coagulation factor
35	225.5	8.7	291	2 I38098	c-plasminogen acti
36	217	8.3	937	2 A45082	neurotrophic recep
37	204	7.8	655	1 A46688	hepatocyte growth
38	195	7.5	615	1 KFHU12	coagulation factor
39	192.5	7.4	558	2 JCS878	plasma hyaluronan-
40	189	7.3	593	2 S45281	coagulation factor
41	186.5	7.2	560	1 JCS795	plasma hyaluronan-
42	182	7.0	806	2 T18840	hypothetical prote
43	159	6.1	685	1 A48289	neurotrophic recep
44	158.5	6.1	433	1 JN0560	u-plasminogen acti
45	158	6.1	442	1 UKPG	u-plasminogen acti

## ALIGNMENTS

## RESULT 1

JH0579  
hepatocyte growth factor precursor [validated] - human  
N:Alternate names: hepatolein A; scatter factor  
C:Species: Homo sapiens (man)  
C>Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #ext change 09-Jul-2004  
C:Accession: JH0579; J00333; A41140; B36677; A36677; A3512; A39006; PH0114; A37796; S06  
R:Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.  
Gene 102, 213-219, 1991  
A:Title: Organization of the human hepatocyte growth factor-encoding gene.  
A:Reference number: JH0579; MUID:91340155; PMID:1831432  
A:Accession: JH0579  
A:Molecule type: DNA  
A:Residues: 1-728 <SEK>  
A:Cross-references: UNIPROT:P14210; DDBJ:D90318  
A:Note: the authors translated the codon GAA for residue 662 as Gly  
R:Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.  
submitted to JIPID, March 1991  
A:Description: Organization of the human hepatocyte growth factor-encoding gene.  
A:Reference number: J00333  
A:Accession: J00333  
A:Molecule type: DNA  
A:Residues: 1-481, RT, 484-728 <SE2>  
R:Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekekerckhove, J.; Weingart, S.; Rieder, H.  
Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991  
A:Title: Evidence for the identity of human scatter factor and human hepatocyte growth f  
A:Reference number: A41140; MUID:91334393; PMID:1831266  
A:Accession: A41140  
A:Molecule type: mRNA  
A:Residues: 1-728 <WEI>  
A:Cross-references: GB:M73239; NID:9337935; PIDN:AA64239.1; PID:9337936  
R:Seki, T.; Ihara, I.; Sugimura, A.; Shimomishi, M.; Nishizawa, T.; Asami, O.; Hagiya, T  
Biochem. Biophys. Res. Commun. 172, 321-327, 1990  
A:Title: Isolation and expression of cDNA for different forms of hepatocyte growth fact  
A:Reference number: A36677; MUID:91025062; PMID:2145836  
A:Accession: B36677  
A:Molecule type: mRNA  
A:Residues: 1-728 <SE3>  
A:Cross-references: GB:M60718; NID:9184031; PIDN:AA52648.1; PID:9184032  
A:Accession: A36677  
A:Molecule type: mRNA  
A:Residues: 1-161, 167-728 <SE4>  
A:Cross-references: EMBL:X16323  
A:Experimental source: leukocyte  
R:Watazawa, K.; Tsudouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakay  
Biochem. Biophys. Res. Commun. 163, 967-973, 1989  
A:Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fac  
A:Reference number: A3512; MUID:89392017; PMID:2528952  
A:Accession: A3512  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-728 <MIY>

A:Cross-references: GB:M29145; NID:G184041; PIDN:AAA52650.1; PID:G306846  
R:Rubin, J.S.; Chan, A.M.L.; Borzato, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hix  
Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991  
A:Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of heparocyte  
A:Reference number: A39006; MUID:91110540; PMID:1824873  
A:Accession: A39006  
A:Molecule type: mRNA  
A:Residues: 1-161,167-728 <RUB>  
A:Cross-references: GB:M55379  
A:Experimental source: embryonic lung  
R:Yoshiyama, Y.; Atakakti, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama,  
Biochem. Biophys. Res. Commun. 175, 660-667, 1991  
A:Title: Identification of the N-terminal residue of the heavy chain of both native and  
A:Reference number: PH0114; MUID:91207365; PMID:1826837  
A:Accession: PH0114  
A:Molecule type: protein  
A:Residues: 32-43;53-58 <YOS>  
A:Experimental source: plasma  
R:Weidner, K.M.; Behrens, J.; Vandekekerckhove, J.; Birchmeier, W.  
J. Cell Biol. 111, 2097-2108, 1990  
A:Title: Scatter factor: molecular characteristics and effect on the invasiveness of epi  
A:Reference number: A37796; MUID:91035621; PMID:2146276  
A:Accession: A37796  
A:Molecule type: protein  
A:Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'X',5  
R:Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimomishi, M.; Sugimura, A.; Tash  
Nature 342, 440-443, 1989  
A:Title: Molecular cloning and expression of human hepatocyte growth factor.  
A:Reference number: S06794; MUID:90066676; PMID:2531289  
A:Accession: S06794  
A:Molecule type: mRNA  
A:Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'M',301-316,'A',318-335,'K',337-386,'  
A:Cross-references: EMBL:X16323; NID:G32081; PIDN:CAA34387.1; PID:G32082  
A:Experimental source: liver  
A>Note: the authors translated the codon CAG for residue 727 as Glu  
A>Note: part of this sequence, including the amino end of both the alpha and beta chains  
R:Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchm  
Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992  
A:Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact  
A:Reference number: I59214; MUID:93087571; PMID:1280830  
A:Accession: I59214  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-288,'ET',<HAR>  
A:Cross-references: GB:I02931; NID:G184033; PIDN:AAA52649.1; PID:G184034  
R:Miyaizawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.  
Eur. J. Biochem. 197, 15-22, 1991  
A:Title: An alternatively processed mRNA generated from human hepatocyte growth factor g  
A:Reference number: S15443; MUID:91200041; PMID:1826653  
A:Accession: S15443  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-288,'ET',<MTY2>  
A:Cross-references: EMBL:X57574; NID:G32083; PIDN:CAA40802.1; PID:G32084  
R:Shima, N.; Nagaoka, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.  
Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991  
A:Title: Tumor cytoxic factor/hepatocyte growth factor from human fibroblasts: cloning  
A:Reference number: I52253; MUID:92062058; PMID:1835583  
A:Accession: I52253  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 161-166 <SH1>  
A:Cross-references: GB:S62561; NID:G237996; PIDN:AA820169.1; PID:G237997  
A:Accession: S62561  
A:Status: preliminary  
A:Residues: 1-728 <SAS2>  
A:Cross-references: GDB:127524; OMIM:142409  
A:Map position: 7q21.1-7q21.1  
A:Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1; 48  
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C:Function: stimulates mitosis of hepatocytes and other cells  
A:Note: does not have proteinase activity  
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1, kringlike homolo

C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringlike; pyr  
F.1-31/Domain: signal sequence #status predicted <SIG>  
F.32-494/495-728/Product: hepatocyte growth factor #status experimental <MAT>  
F.332-494/Domain: alpha chain #status experimental <ACH>  
F.128-206/Domain: kringlike homology <KR1>  
F.211-288/Domain: kringlike homology <KR2>  
F.305-383/Domain: kringlike homology <KR3>  
F.391-469/Domain: kringlike homology <KR4>  
F.495-728/Domain: beta chain #status experimental <BCH>  
F.495-716/Domain: trypsin homology <TRY>  
F.332/Modified site: pyrolicone carboxylic acid (Gln) (in mature form) #status experimen  
F.294/402,566,653/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F.487-604/Disulfide bonds: #status predicted

Query Match 99.9%; Score 2601; DB 1; Length 728;  
Best Local Similarity 99.8%; Pred. No. 1,9e-176;  
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ERKRNTIHERFKSAKTLIKIDPALKIKTKVNTADGCANRCTRNKGLPFTCKAFVFDK 60  
DB 32 QRKRNTIHERFKSAKTLIKIDPALKIKTKVNTADGCANRCTRNKGLPFTCKAFVFDK 91  
QY 61 ARKQCLMPFNSMSGVKKEGFEDLYENDDYRNCILIGRSGYKGVSTTKSGIKOP 120  
DB 92 ARKQCLMPFNSMSGVKKEGFEDLYENDDYRNCILIGRSGYKGVSTTKSGIKOP 151  
QY 121 WSMNIPHEHSFLPSSYRKDLOENYCRNPRGEGGPMCFSTNPEYRVCDIPOCSEYEC 180  
DB 152 WSMNIPHEHSFLPSSYRKDLOENYCRNPRGEGGPMCFSTNPEYRVCDIPOCSEYEC 211  
QY 181 MTCNGESYRGLMDHTESGKICQRMDOHQTPHRHKLPERYPDKGPDNDYCRNPDGCPRWC 240  
DB 212 MTCNGESYRGLMDHTESGKICQRMDOHQTPHRHKLPERYPDKGPDNDYCRNPDGCPRWC 271  
QY 241 YTLDPHTWEYCAIKTCADNTMDTVLETTTECICQGGEGYRGTVNTVNGICQQRDS 300  
DB 272 YTLDPHTWEYCAIKTCADNTMDTVLETTTECICQGGEGYRGTVNTVNGICQQRDS 331  
QY 301 QYPHEHDTPNPFCKDIRENYCRNPDGSESPMCFPTDPNIRVGCSSQIPNCDSHGQDC 360  
DB 332 QYPHEHDTPNPFCKDIRENYCRNPDGSESPMCFPTDPNIRVGCSSQIPNCDSHGQDC 391  
QY 361 YRNGKNYMGSLQTRSGLTCSMDKNMEDLHRHIFWEPDASKLNNYCRNPDGAGPW 420  
DB 392 YRNGKNYMGSLQTRSGLTCSMDKNMEDLHRHIFWEPDASKLNNYCRNPDGAGPW 451  
QY 421 CYTGNPLIPWDYCPISRCGDTPTIV 447  
DB 452 CYTGNPLIPWDYCPISRCGDTPTIV 478

RESULT 2  
A60185  
hepatocyte growth factor precursor - mouse  
N:Alternate names: hepatoleitin A; scatter factor  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Mar-1993 #sequence revision 26-May-1994 #text change 09-Jul-2004  
C:Accession: J02117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758; J02211  
R:Saeki, M.; Nishio, M.; Saeki, T.; Enami, J.  
Biochem. Biophys. Res. Commun. 199, 772-779, 1994  
A:Title: Identification of mouse mammary fibroblast-derived mammary growth factor as hep  
A:Reference number: JC2117; MUID:94183257; PMID:8135822  
A:Accession: JC2117  
A:Molecule type: mRNA  
A:Residues: 1-728 <SAS2>  
A:Cross-references: UNIPROT:O08048; GB:D10212; NID:G220435; PIDN:BA01064.1; PID:G220436  
A:Experimental source: fibroblast, COS-1 cell  
A:Note: submitted to JIPID, May 1993  
A:Accession: PC2064  
A:Molecule type: protein  
A:Residues: 496-504 <SAS2>  
R:Rosen, E.M.; Weimsky, L.; Setter, E.; Winter, D.W.; Goldberg, I.D.  
Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990

A:Title: Purified scatter factor stimulates epithelial and vascular endothelial cell mig  
A:Reference number: A60185; MUID:90377927; PMID:2144630  
A:Accession: A60185  
A:Molecule type: protein  
A:Residues: 'X',184-188,'X','191-192,'X',194,'XX',197,357-364,'XX',367,375-377,'E',379,'  
R:Aliu, Y.; Michalopoulos, G.K.; Zarnegar, R.  
Biochim. Biophys. Acta 1216, 299-303, 1993  
A:Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth  
A:Reference number: S43416; MUID:94060105; PMID:8241272  
A:Accession: S43416  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-728 <Lit>  
A:Cross-references: EMBL:X72307  
R:Aliu, Y.  
submitted to the EMBL Data Library, May 1993  
A:Reference number: S45521  
A:Accession: S45521  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-563,'H',565-728 <Lit>  
A:Cross-references: EMBL:X72307  
R:Cooper, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.  
Biochem. J. 278, 35-41, 1991  
A:Title: Purification and characterization of biologically active scatter factor from ra  
A:Reference number: S17173; MUID:91354223; PMID:1831975  
A:Accession: S17173  
A:Molecule type: protein  
A:Residues: 496-517,'T',519 <COF>  
R:Gherardi, E.; Stoker, M.  
Nature 346, 228, 1990  
A:Title: Hepatocytes and scatter factor.  
A:Reference number: S10966; MUID:90326152; PMID:2142751  
A:Accession: S10966  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 496-507,'X',509-512,'L',514-516,'X',518-519 <MAT>  
R:Plasche-Schluter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.  
J. Biol. Chem. 270, 830-836, 1995  
A:Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.  
A:Reference number: I48758; MUID:95122532; PMID:7822318  
A:Accession: I48758  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-30 <RES>  
A:Cross-references: EMBL:X81630; NID:9673451; PIDN:CA57286.1; PID:9673452  
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C:Function:  
A:Description: stimulates mitosis of hepatocytes and other cells  
A>Note: does not have proteinase activity  
C:Superfamily: hepatocyte growth factor/macrophae stimulating protein 1; kringe homol  
C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringe; pyr  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:56-495/Domain: hepatocyte growth factor #status predicted <MAT>  
F:129-207/Domain: kringe homology <KR1>  
F:212-289/Domain: kringe homology <KR2>  
F:306-384/Domain: kringe homology <KR3>  
F:392-470/Domain: kringe homology <KR4>  
F:496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>  
F:496-719/Domain: trypsin homology <TRY>  
F:33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F:295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:488-607/Disulfide bonds: #status predicted

Query Match 92.5%; Score 2408; DB 1; Length 728;  
Best Local Similarity 91.1%; Pred. No. 8,6e-163;  
Matches 407; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

QY 1 ERKRRTHIEFKSATTTIKIDPAIKTKKYNATDQCNRKRGJLPTCKARVFPK 60  
DB 33 QKRRNTLHEFKSATTTIKEDPLKIKTKYVNSADBCANCRIRNRGFTTCKARVFPK 92

QY 61 ARKQCIWPPPNSSGCVKKEFGHEFDLYENKQYINRCIIIGKRSYKGVITKSGIKCOP 120  
DB 93 SRRCYWPFPNMSGCVKKEFGHEFDLYENKQYINRCIIIGKRSYKGVITKSGIKCOP 152  
QY 121 WRSMT PHRESFLPSSYRGKDLQENYCRNRRGEGGWCFTSNPEVREYCDIPQCEVBC 180  
DB 153 WMSMT PHRESFLPSSYRGKDLQENYCRNRRGEGGWCFTSNPEVREYCDIPQCEVBC 212  
QY 181 MTCNSES YGLMDHRESGKICQRMWDQTPHRRKFLPERYPDGPDPNNYCRNPDGCRPWC 240  
DB 213 MTCNSES YRGPMRDHRESGKICQRMWDQTPHRRKFLPERYPDGPDPNNYCRNPDGCRPWC 272  
QY 241 YTLDPHTMEYCAITCADNTMDTDVPLETTECIQGGEGYRGVTNTWNGIPCORWDS 300  
DB 273 YTLDPHTMEYCAITCADNTMDTDVPLETTECIQGGEGYRGVTNTWNGIPCORWDS 332  
QY 301 QYPHEDMTPEMFKCDLRENYCRNPDGSESWCFTTPNIRVGYCSQIPKCDVSSGQDC 360  
DB 333 QYPHEDMTPEMFKCDLRENYCRNPDGSESWCFTTPNIRVGYCSQIPKCDVSSGQDC 392  
QY 361 YRNGKNYVGNISQTRSGLTCSMDKNMEDLHRHIFWEPDASKLBNRYCRNPDGAGFW 420  
DB 393 YRNGKNYVGNISQTRSGLTCSMDKNMEDLHRHIFWEPDASKLBNRYCRNPDGAGFW 452  
QY 421 CYTGNDLIPWDYCPISRCGEGTTPITV 447  
DB 453 CYTGNDLIPWDYCPISRCGEGTTPITV 479

## RESULT 3

A35644

hepatocyte growth factor precursor - rat

N:Alternate names: hepalectin A; scatter factor

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 28-Sep-1990 #sequence revision 18-Nov-1992 #text change 09-Jul-2004

A:Accession: A35644; S13211

R:Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Shimizu, S.; Nakamura

Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990

A:Title: Deduced primary structure of rat hepatocyte growth factor and expression of the

A:Reference number: A35644; MUID:90222197; PMID:2139229

A:Accession: A35644

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-728 &lt;TAS&gt;

A:Cross-references: UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA41433.1;

A&gt;Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417

R:Okajima, A.; Miyazawa, K.; Kitamura, N.  
Eur. J. Biochem. 193, 375-381, 1990

A:Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA dur

A:Accession: S13211; MUID:91031482; PMID:2146117

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-728 &lt;OKA&gt;

A:Cross-references: EMBL:X54400; NID:956353; PIDN:CA38266.1; PID:94539554

C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor

C:Function:  
A:Description: stimulates mitosis of hepatocytes and other cells

A&gt;Note: does not have proteinase activity

C:Superfamily: hepatocyte growth factor/macrophae stimulating protein 1; kringe homol

C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringe; pyr

F:1-32/Domain: signal sequence #status predicted &lt;SIG&gt;

F:56-495/Domain: hepatocyte growth factor #status predicted &lt;MAT&gt;

F:129-207/Domain: kringe homology &lt;KR1&gt;

F:212-289/Domain: kringe homology &lt;KR2&gt;

F:306-384/Domain: kringe homology &lt;KR3&gt;

F:392-470/Domain: kringe homology &lt;KR4&gt;

F:496-728/Domain: hepatocyte growth factor beta chain #status predicted &lt;BCH&gt;

F:496-719/Domain: trypsin homology &lt;TRY&gt;

F:33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

F:295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:488-607/Disulfide bonds: #status predicted

Query Match 92.2%; Score 2401; DB 1; Length 728;  
Best Local Similarity 90.4%; Pred. No. 2,7e-162;  
Matches 404; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

```
QY 1 EKRNRNTHPEPKSAKTTLIKIDPALKIKTKKVNNTADOCANCTRNKGLPFTCKAFVFDK 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 33 QKRNRNTHPEPKSAKTTLIKIDPALKIKTKKVNNTADOCANCTRNKGLPFTCKAFVFDK 92
QY 61 ARKCLMPFNSSSGVKKFEGHEPDLVENKDYINRCIIIGKRSYKGVTSITKSGIKOP 120
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 93 SKRCLWTPFNSSSGVKKFEGHEPDLVENKDYINRCIIIGKRSYKGVTSITKSGIKOP 152
QY 121 WSMSTPHEHSFLPSSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDDIPQSEVEVC 180
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 153 WMSMTPEHSFLPSSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDDIPQSEVEVC 212
QY 181 MTCNGESYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDDIPQSEVEVC 240
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 213 MTCNGESYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDDIPQSEVEVC 272
QY 241 YLDPHTRWECALIKTCADNTMNDTDVPLETTECIIQGGEGYRGVTNTIWNGLPCORWDS 300
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 273 YLDPHTRWECALIKTCADNTMNDTDVPLETTECIIQGGEGYRGVTNTIWNGLPCORWDS 332
QY 301 QYRPHEDMTPEPKCKDLRENYCRNPDGSGSPCFTTDPNIRVGYCSQIPNCDSHGQDC 360
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 333 QYRPHGKDTPEPKCKDLRENYCRNPDGSGSPCFTTDPNIRVGYCSQIPNCDSHGQDC 392
QY 361 YRNGKKNYMGNTLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLANTENYCRNPDGAGW 420
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 393 YRNGKKNYMGNTLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLANTENYCRNPDGAGW 452
QY 421 CYTGNPLIPMDYCPISRCGDTPTTIV 447
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 453 CYTGNPLIPMDYCPISRCGDTPTTIV 479
```

## RESULT 4

151283  
hepatocyte growth factor precursor - clawed frog  
N/Alternate names: hepatocytin A; scatter factor  
C/Species: Xenopus sp. (clawed frog)  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-May-2004  
C/Accession: I51283  
R.Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiohara, K.  
Meth. Dev. 49, 123-131, 1995  
A/Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus ear  
A/Reference number: I51283; MUID:95267690; PMID:7748783  
A/Accession: I51283  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-710 <NA>  
A/Cross-references: GB:S77422; NID:9998932; PIDN:AB34354.1; PID:9998933  
A/Note: the authors' translation for residue 458 (Thr) is inconsistent with the nucleoti  
C/Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C/Function:  
A/Description: stimulates mitosis of hepatocytes and other cells  
A/Note: Does not have proteinase activity  
C/Superfamily: hepatocyte growth factor/macrophage stimulating protein 1, kringle homo  
C/Keywords: duplication; glycoprotein; growth factor; heterodimer; kringle  
F:42-477/478-709/Product: hepatocyte growth factor #status predicted <Mat>  
F:42-477/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>  
F:115-193/Domain: kringle homology <KR1>  
F:198-275/Domain: kringle homology <KR2>  
F:289-367/Domain: kringle homology <KR3>  
F:375-453/Domain: kringle homology <KR4>  
F:478-709/Domain: hepatocyte growth factor beta chain #status predicted <BCH>  
F:478-709/Domain: trypsin homology <TRY>  
F:52-128,281,322,379,550,637,666/Binding site: carbohydrate (Asn) (covalent) #status pre  
F:470-588/Disulfide bonds: #status predicted

Query Match 71.6%; Score 1864.5; DB 1; Length 710;

Best Local Similarity 69.3%; Pred. No. 2.3e-124;  
Matches 305; Conservative 64; Mismatches 68; Indels 3; Gaps 1;

```
QY 3 KRRNTHPEPKSAKTTLIKIDPALKIKTKKVNNTADOCANCTRNKGLPFTCKAFVFDKAR 62
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 21 KRRNTHPEPKSAKTTLIKIDPALKIKTKKVNNTADOCANCTRNKGLPFTCKAFVFDK 80
QY 63 KCLMPFNSSSGVKKFEGHEPDLVENKDYINRCIIIGKRSYKGVTSITKSGIKOPWS 122
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 81 KCHWPSFNTMSAGIKKDYISFDLYEKDYLRCICIHGKSNVGTNRVTKRGLACQPMN 140
QY 123 SMITHESFLPSSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDDIPQSEVEVCMT 182
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 141 SMITHESFLPSSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDDIPQSEVEVCMT 200
QY 183 CNGESYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDDIPQSEVEVCMT 242
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 201 CNGESYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDDIPQSEVEVCMT 260
QY 243 LDPHTRWECALIKTCADNTMNDTDVPLETTECIIQGGEGYRGVTNTIWNGLPCORWDS 302
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 261 LDPHTRWECALIKTCADNTMNDTDVPLETTECIIQGGEGYRGVTNTIWNGLPCORWDS 317
QY 303 PHEHDMTPENPKCKDLRENYCRNPDGSGSPCFTTDPNIRVGYCSQIPNCDSHGQDCYR 362
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 318 PHLNHFPEPNYCKDLSENYCRNPDGSGSPCFTTDPNIRVGYCSQIPNCDSHGQDCYR 377
QY 363 GNGKKNYMGNTLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLANTENYCRNPDGAGW 422
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 378 GNGKKNYMGNTLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLANTENYCRNPDGAGW 437
QY 423 TGNPLIPMDYCPISRCGDT 442
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 438 TGNPLIPMDYCPISRCGDT 457
```

## RESULT 5

151285  
hepatocyte growth factor/scatter factor - chicken (fragment)  
C/Species: Gallus gallus (chicken)  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C/Accession: I51285  
R.Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Cherard  
Development 121, 813-824, 1995  
A/Title: A role for HGF/SF in neural induction and its expression in Hensen's node durin  
A/Reference number: I51285; MUID:95237013; PMID:7720585  
A/Accession: I51285  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-411 <STR>  
A/Cross-references: UNIPROT:Q90978; GB:S77480; NID:9998675; PID:9998676  
C/Superfamily: hepatocyte growth factor/macrophage stimulating protein 1, kringle homo  
F:124-197/Domain: kringle homology <KR2>  
F:202-279/Domain: kringle homology <KR3>  
F:296-374/Domain: kringle homology <KR3>

Query Match 66.7%; Score 1737.5; DB 2; Length 411;  
Best Local Similarity 74.9%; Pred. No. 1.3e-115;  
Matches 289; Conservative 47; Mismatches 45; Indels 5; Gaps 1;

```
QY 3 KRRNTHPEPKSAKTTLIKIDPALKIKTKKVNNTADOCANCTRNKGLPFTCKAFVFDKAR 62
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 30 KRRNTHPEPKSAKTTLIKIDPALKIKTKKVNNTADOCANCTRNKGLPFTCKAFVFDK 89
QY 63 KCLMPFNSSSGVKKFEGHEPDLVENKDYINRCIIIGKRSYKGVTSITKSGIKOPWS 122
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 90 KCHWPSFNTMSAGIKKDYISFDLYEKDYLRCICIHGKSNVGTNRVTKRGLACQPMN 149
QY 123 SMITHESFLPSSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDDIPQSEVEVCMT 182
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 150 SMITHESFLPSSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDDIPQSEVEVCMT 204
QY 183 CNGESYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDDIPQSEVEVCMT 242
```



```

QY      213 KFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDLPHTRMEYCAIKTCADN-----TMNDT 265
      224 PFQPEKFLDKLDKQNYCGRNPDGSEKRPWCYTLDPNVEREFCDLPSCGPNLPPTTKSKSQ 283
QY      266 DVPLETTECTIGOGEGRYGTYNTWNGIPQGRMSQYRPHEDMTPEPKCKDLRENYCRN 325
      284 RNKVASLNCFRGKGEDYRGTYNTTSAGVPCQRMWAQSHQRFVPEKCYACKDLRENYCRN 343
QY      326 PDGSEPMCFCTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKMYGNLSQTRSGLTCSMW 384
      344 PDGSEPMCFCTSRRLRMAFCHQIPRCTBELVPCGCHYSGSEGYRGSKYKRGVQCQHM 403
Db      404 --SSETPHKPQFTPTSPAPAGLEANFCRNPDPGDSHGPMWCYTLDLFDYCALRCDDDQ 461
QY      443 TPPTIV 447
      462 PPSIL 466
Db

```

## RESULT 8

```

A40332
macrophage-stimulating protein 1 precursor - mouse
N:Alternate names: hepatocyte growth factor-like protein
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: A40332; B40332
R:Deegen, S.U.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
Biochemistry 30, 9781-9791, 1991
A>Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth fact
A:Reference number: A40332; MUID:92002017; PMID:1832957
A:Accession: A40332
A:Molecule type: DNA
A:Residues: 1-716 <DEG>
A:Cross-references: UNIPROT:P29628; GB:M74180; NID:g193831; PIDN:AAA50166.1; PID:g193832
A:Accession: B40332
A:Molecule type: mRNA
A:Residues: 1-18,'p',20-716 <DEG>
A:Cross-references: GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g193834
C:Genetics:
A:introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/1; 412/2; 458/1; 47
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C:Keywords: duplication; glycoprotein; growth factor; kringle
F:1-31/Domain: signal sequence #status predicted <SIG>
F:19-488,489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>
F:119-483/Domain: alpha chain #status experimental <ACH>
F:110-186/Domain: kringle homology <KR1>
F:191-268/Domain: kringle homology <KR2>
F:292-370/Domain: kringle homology <KR3>
F:379-457/Domain: kringle homology <KR4>
F:484-711/Domain: beta chain #status experimental <BCH>
F:489-709/Domain: trypsin homology <TRY>
F:172,173,305,620/Binding site: carbohydrate (asn) (covalent) #status predicted

```

```

Query Match      43.2%; Score 1125; DB 1; Length 716;
Best Local Similarity 45.9%; Pred. No. 4,7e-72;
Matches 195; Conservative 69; Mismatches 143; Indels 18; Gaps 6;

QY      33 VNTADCANRCTENKGLPTCKAFVDEKARKOCLMPFPNMSGSGVKKERGFEDLYENKD 92
      50 VADAECCARRC-----GRLDCAFAHNMSSHCQLLPWQHSLHQLYHSSLCILFQKDD 105
Db      93 YVRNCTIGKRGSYKTVSTKSGIKCOQPMSSMIPHEHSLPSSYRGKDLQENYCRNPGE 152
      106 YVRTCIMDNGVSYRGTVARTAGGLPCQAMSRPFPNDHKYTPPKNG--LEENFCRNPDD 163
QY      153 EGGPMCFSTNPFRVYVCIPQSEVECMTCNGESRGIMDHESGKICORDMHCQPHH 212
      164 PRGPMCYTTNRSYVFOSCGIKTCREAVCYLCSNEDYRGVEDYSGRECRMDLQPHSH 223
Db

```

```

QY      213 KFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDLPHTRMEYCAIKTCADN-----TMNDT 265
      224 PFQPEKFLDKLDKQNYCGRNPDGSEKRPWCYTLDPNVEREFCDLPSCGPNLPPTTKSKSQ 283
QY      266 DVPLETTECTIGOGEGRYGTYNTWNGIPQGRMSQYRPHEDMTPEPKCKDLRENYCRN 325
      284 RNKVASLNCFRGKGEDYRGTYNTTSAGVPCQRMWAQSHQRFVPEKCYACKDLRENYCRN 343
QY      326 PDGSEPMCFCTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKMYGNLSQTRSGLTCSMW 384
      344 PDGSEPMCFCTSRRLRMAFCHQIPRCTBELVPCGCHYSGSEGYRGSKYKRGVQCQHM 403
Db      404 --SSETPHKPQFTPTSPAPAGLEANFCRNPDPGDSHGPMWCYTLDLFDYCALRCDDDQ 461
QY      443 TPPTIV 447
      462 PPSIL 466
Db

```

## RESULT 9

```

PRPG
plasmin (EC 3.4.21.7) precursor - pig (fragment)
N:Alternate names: plasminogen
N:Contains: miniplasminogen
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: S03733; S03737; A25834
R:Schaller, J.; Marti, T.; Roesseler, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A>Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca
A:Reference number: S03733
A:Accession: S03733
A:Molecule type: protein
A:Residues: 1-560 <SCH>
A:Cross-references: UNIPROT:P06667
R:Brundishol, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Leigier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A>Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A:Reference number: S03735; MUID:81212097; PMID:7238497
A:Accession: S03737
A:Molecule type: protein
A:Residues: 1-57 <BRU>
R:Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
A>Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A:Reference number: A25834; MUID:85203907; PMID:3846533
A:Accession: A25834
A:Molecule type: protein
A:Residues: 450-790 <MAR>
C:Function:
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A:Pathway: fibrinolysis
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote
F:1-790/Product: plasminogen #status predicted <PRO>
F:1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
F:1-77/Domain: activation peptide #status predicted <AP>
F:78-560/Product: plasmin chain A #status predicted <ACH>
F:166-243/Domain: kringle homology <KR1>
F:256-333/Domain: kringle homology <KR2>
F:358-435/Domain: kringle homology <KR3>
F:450-790/Product: miniplasminogen #status experimental <MIN>
F:461-540/Domain: kringle homology <KR5>
F:561-790/Product: plasmin chain B #status experimental <BCH>
F:561-783/Domain: trypsin homology <TRY>
F:30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305
bonds: #status predicted
F:602,645,740/Active site: His, Asp, Ser #status predicted

```



C-Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydrolysis; plasminogen-related protein precursor homology <PLHP>

F:1-96/Domain: plasminogen-related protein precursor homology <SIG>

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-812/Product: plasminogen #status predicted <PRO>

F:20-96/Domain: activation peptide #status predicted <APT>

F:79-466/Product: angiotensin #status predicted <AS7>

F:97-581,582-812/Product: plasmin #status predicted <MAT>

F:97-581/Domain: chain A #status predicted <ACH>

F:103-181/Domain: kringle homology <KR1>

F:185-262/Domain: kringle homology <KR2>

F:275-352/Domain: kringle homology <KR3>

F:377-454/Domain: kringle homology <KR4>

F:481-560/Domain: kringle homology <KR5>

F:582-812/Domain: chain B #status predicted <BCH>

F:582-812/Domain: trypsin homology <TRY>

F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,320-352/Status: predicted

F:78-79/Cleavage site: Glu-Asn (seromelysin 1) #status predicted

F:136,308/Binding site: carboxylate (Asn) (covalent) #status predicted

F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted

F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental

F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match	40.7%	Score 1059	DB 1	Length 812
Best Local Similarity	43.3%	Pred. No. 2.5e-67		
Matches	191	Conservative 67	Mismatches 145	Indels 38
				Gaps 12

30 TKKVNTA---DOCANRCTRNGKGLPTCKAFNFDKARQCLWFFPNSMSGVKKKEGHEFD 86

37 TKQOLAAGVSDCLACEGE--TDVCRSFQYHNSKEDQCVIAENSKTSSIIIR--RDVI 92

87 IYENKDVIYRNCIIIGKRSYKGVTSITKSGIKQCPWSSMIPIHEHSFLPSSYRGKDLQENYC 146

93 LFEKRYVYLSECKTGKIGNGYRGATMSRTKSGVACQKMGATFPHPVNYSPSTHPNEGLENNYC 152

147 RNPREGEGPWCNTSNPEVRYEVCDFQCSEFEVCMTNGESYRGMLDHTESKICQRMWH 206

153 RNPNDDEQGPWCCTTDPDKRYDCNIPCEBE--ECMYSGEYEGKISIKTSLDQWADS 211

207 QTPHRHKFPERPDYDGFDDNYCRNPDGPSPWCYTLDLPHRMEXCAIKTCADNTMNDID 266

212 QSPHAGHYIPAKFPSSKMLKNNYCHNPDEBERPWCFTTDPTRKWEYCDIPRCT---TPRP 267

267 VPLETTECIQOGEGYRGTVNTIWMGIPCORWDSQYPHEHDMTPENFKCKDLRENYCRNP 326

268 PSPPTQCLKRGRENYRGTVSVTSVSGKTCQWWSQTPHRHNRTPENFPCKNLENNYCRNP 327

327 DGSSESWCCTTDPNIVGVYSQIPLNCDSHG-----QDCYRGKKNYM 369

328 DDETAFWCYTTDSQLWEYEC--EIPSCSSASPDSDSSVPPEEQTPVVOECQSDGOSYR 386

370 GNLSOTRSGGLTCSMWKNNMEDLRHIFWE---PASKLINENYCRNPDADAGPWCYCTNP 426

387 GTSSTTTTIGKCKOSWAMMP--HRHSKTPENFPDAG--LENNYCRNPDG--KGPWCYTTPD 442

427 LIPWDYCPISRCGEGDTTPPIV 447

443 SVRWECYCNLKRCC--SETGGSYV 462

RESULT 11

146260

plasmin (EC 3.4.21.7) Precursor - western European hedgehog CSpecies: Erinaceus europaeus (western European hedgehog) CDate: 21-Feb-1997 #sequence\_rev150 21-Feb-1997 #text\_change 09-Jul-2004 CAccession: I46260

R:Lawm, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fom J. Biol. Chem. 270, 24004-24009, 1995

A:Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein A:Reference number: I46259; PMID:96025778; PMID:7592597

A:Accession: I46260

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA



A:Molecule type: mRNA  
 A:Residues: 1-471,'D',473-810 <FOR>  
 A:Cross-references: GB:X05199; NID:935530; PIDN:CAA28831.1; PID:935531  
 A:Experimental source: liver  
 R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.  
 Biochemistry 23, 4243-4250, 1984  
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and  
 A:Reference number: 145961; PMID:85023311; PMID:6148961  
 A:Accession: 162738  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 292-471,'D',473-810 <MAL2>  
 A:Cross-references: GB:X02922; NID:9190112; PIDN:AAA60124.1; PID:9387031  
 A:Accession: 184609  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 367-419 <MAL3>  
 A:Cross-references: GB:X02921; NID:9190110; PIDN:AAA60123.1; PID:9190111  
 R:Brundisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;  
 Eur. J. Biochem. 114, 465-470, 1981  
 A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,  
 A:Reference number: S03735; PMID:81212097; PMID:7238497  
 A:Accession: S03735  
 A:Molecule type: protein  
 A:Residues: 20-71,'E',73-76 <BRU>  
 R:Sortrup-Jensen, L.; Petersen, T.E.; Magnusson, S.  
 submitted to the Atlas, July 1977  
 A:Reference number: A00929  
 A:Accession: A00929  
 A:Molecule type: protein  
 A:Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOR>  
 R:Wiman, B.  
 Eur. J. Biochem. 76, 129-137, 1977  
 A:Title: Primary structure of the B-chain of human plasmin.  
 A:Reference number: A04627; PMID:77225245; PMID:142009  
 A:Accession: A04627  
 A:Molecule type: protein  
 A:Residues: 581-810 <W1>  
 R:Wiman, B.; Wallen, P.  
 Eur. J. Biochem. 50, 489-494, 1975  
 A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human pla  
 A:Reference number: A04625; PMID:75093329; PMID:122932  
 A:Accession: A04625  
 A:Molecule type: protein  
 A:Residues: 20-50,'Q',51-71,'E',73-85,87-100 <W2>  
 R:Wiman, B.; Wallen, P.  
 Eur. J. Biochem. 58, 539-547, 1975  
 A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha  
 A:Reference number: A04626; PMID:76043692; PMID:126863  
 A:Accession: A04626  
 A:Molecule type: protein  
 A:Residues: 483-507,'E',509-604 <W13>  
 R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summari, L.  
 J. Biol. Chem. 248, 1631-1633, 1973  
 A:Title: The primary structure of human plasminogen. II. The histidine loop of human pla  
 A:Reference number: A92125; PMID:73149248; PMID:4694729  
 A:Contents: annotation; active site  
 R:Grozkopf, W.R.; Summari, L.; Robbins, K.C.  
 J. Biol. Chem. 244, 3590-3597, 1969  
 A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of a  
 A:Reference number: A92048; PMID:69234739; PMID:4420117  
 A:Contents: annotation; active site  
 R:Trexler, M.; Vail, Z.; Patchy, L.  
 J. Biol. Chem. 257, 7401-7406, 1982  
 A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.  
 A:Reference number: A92382; PMID:82213905; PMID:6919539  
 A:Contents: annotation; omega-aminocarboxylic acid binding sites  
 R:Vail, Z.; Patchy, L.  
 J. Biol. Chem. 259, 13690-13694, 1984  
 A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential  
 A:Reference number: A92459; PMID:85054794; PMID:6094526  
 A:Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site

R:Caio, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.  
 J. Biol. Chem. 271, 29461-29467, 1996  
 A:Title: Kring domains of human angiotensin. Characterization of the anti-proliferati  
 A:Reference number: A58811; PMID:97067211; PMID:8910613  
 A:Contents: annotation  
 R:Uljen, H.R.; Ugwu, F.; Bini, A.; Collen, D.  
 Biochemistry 37, 4699-4702, 1998  
 A:Title: Generation of an angiotensin-like fragment from plasminogen by streptolysin-1  
 A:Reference number: A58812; PMID:9548733; PMID:9548733  
 A:Contents: annotation  
 R:Tulinsky, A.; Mulichak, A.M.  
 submitted to the Brookhaven Protein Data Bank, July 1991  
 A:Reference number: A51341; PDB:1PMK  
 A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454  
 R:Tulinsky, A.; Wu, T.P.  
 submitted to the Brookhaven Protein Data Bank, July 1991  
 A:Reference number: A51488; PDB:2PKA  
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454  
 R:Wu, T.P.; Tulinsky, A.  
 submitted to the Brookhaven Protein Data Bank, August 1993  
 A:Reference number: A51911; PDB:1PMK  
 A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181  
 R:Padmanabhan, K.; Tulinsky, A.  
 submitted to the Brookhaven Protein Data Bank, April 1994  
 A:Reference number: A52408; PDB:1PMK  
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454  
 R:Tulinsky, A.; Mathews, I.I.  
 submitted to the Brookhaven Protein Data Bank, August 1993  
 A:Reference number: A65244; PDB:1CEA  
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181  
 R:Tulinsky, A.; Mathews, I.I.  
 submitted to the Brookhaven Protein Data Bank, December 1995  
 A:Reference number: A65245; PDB:1CEB  
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181  
 R:Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.  
 Biochemistry 30, 10576-10586, 1991  
 A:Title: Crystal and molecular structure of human plasminogen kring 4 refined at 1.9 Å  
 A:Reference number: A58819; PMID:92031502; PMID:1657148  
 A:Contents: annotation  
 R:Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.  
 Biochemistry 30, 10589-10594, 1991  
 A:Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmi  
 A:Reference number: A58818; PMID:92031503; PMID:1657149  
 A:Contents: annotation  
 R:de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M  
 Biochemistry 31, 270-279, 1992  
 A:Title: Crystal structure of the kring 2 domain of tissue plasminogen activator at 2  
 A:Reference number: A39483; PMID:92118803; PMID:1310033  
 A:Contents: annotation; X-ray crystallography, 2.4 angstroms  
 R:Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.  
 submitted to the Brookhaven Protein Data Bank, June 1995  
 A:Reference number: A65980; PDB:1KRN  
 A:Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454  
 R:Rejzante, M.; Llinas, M.  
 submitted to the Brookhaven Protein Data Bank, August 1996  
 A:Reference number: A65803; PDB:1HPJ  
 A:Contents: annotation; conformation by (1)H-NMR, residues 103-181  
 R:Rejzante, M.; Llinas, M.  
 submitted to the Brookhaven Protein Data Bank, August 1996  
 A:Reference number: A65804; PDB:1HPK  
 A:Contents: annotation; conformation by (1)H-NMR, residues 103-181  
 R:Rejzante, M.R.; Llinas, M.  
 Eur. J. Biochem. 221, 939-949, 1994  
 A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasmin  
 A:Reference number: A58817; PMID:94237158; PMID:8181476  
 A:Contents: annotation; conformation by (1)H-NMR  
 C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many o  
 C:Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU



Db 158 YCNPNNDENGPWCYTTPDDPKRYDCDIEPC-EDKCMHCSGENYEKIAWTMSGRCQAM 216  
QY 205 DHQTPRHKFLPRRYDCKGDDNVCNPNPGOPRPMWCTTLDPHRWVCATKTCADMTMND 264  
Db 217 DSQSPAHAGYIYSKFPNKKLKNMYCRNPDEPRPCPTDPQKRWECDDPCT----- 270  
QY 265 TDVPLE--TTECTIOGEGYRGTVNTIWNIGIPCORWDSQYPHEDMTPEHFCKDLRENY 322  
Db 271 TPEPSGPRYQCLKGTGKNYGGVAVATESGHTQORWSEQTPHKHRTPEHFCKDLRENY 330  
QY 323 CRNPDSGSESPWCTTDPNIRVGYCSQIPNCDMSH-----GDCYRGNG 365  
Db 331 CRNPNEKAPWCYTTNSVWRMEYCT-IPSCSSPLSTERMDVVPPEQTVPVQDCYHGNG 389  
QY 366 KNYMGLSQTRSGLTCSMDKNMEDLHRHFWME--PDASKLNENYCRNPDDDAHGPMW 422  
Db 390 QSTRGTSSTTITRKQCSWSMTP--HRHLKTPENYPNAG-LTMNYCRNPDDAD-KSPWCY 445  
QY 423 TGNPLIPMDYCPISRC 438  
Db 446 TTDPRVRWEFCNLKCC 461

## RESULT 15

T18518  
apolipoprotein(a) - western European hedgehog (fragment)  
C:Species: Erinaceus europaeus (western European hedgehog)  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18518  
R:Jawm, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong, J. Biol. Chem. 270, 24004-24009, 1995  
A:Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein A:Reference number: I46259; PMID:96025778; PMID:7592597  
A:Accession: T18518  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2869 <LAW>  
A:Cross-references: UNIPROT:Q28398; EMBL:U33170; NID:g1046358; PID:g1046359; PIDN:AAC485  
A:Experimental source: liver  
C:Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, contains apolipoprotein(a).

Query Match 36.2%; Score 943.5; DB 2; Length 2869;  
Best Local Similarity 45.6%; Pred. No. 1,4e-58;  
Matches 173; Conservative 51; Mismatches 126; Indels 29; Gaps 10;

QY 89 ENKDYTRNCIIIGKRSYKGTVSTIKSGIKQPMWSMI PHEHSFLPSSYRGKDLQENYCRN 148  
Db 2490 EPLDLVDQCLEGTGENYRGMAVTASGHTCQWRREQSPHSRTPENYPTKNLVGNVCRN 2549  
QY 149 PRGEGGPMCTNSNPRVYECDIPOCS-----VEGMCNGESYRGLMDHTS 197  
Db 2550 PGEV-APWCYTTNSAMRWEYCSIPACESPTPTLHVPEQCLENGENYQGNMAITVS 2608  
QY 198 GKICQRMWDQTPRHKFLPRRYDCKGDDNVCNPNPGOPRPMWCTTLDPHRWVCATKTC 257  
Db 2609 GPCQGMKQTPRHKFLPRRYDCKGDDNVCNPNPGOPRPMWCTTLDPHRWVCATKTC 2668  
QY 258 ADNTMNDTVPLETTCTIOGEGYRGTVNTIWNIGIPCORWDSQYPHEDMTPEHFCKDX 317  
Db 2669 -ESSSPTEPMIIPDQCLRGTEYRGSAVAVTASGHTCQWRREQSPHSRTPENYPTKN 2727  
QY 318 LRENYCRNPDSGSESPWCTTDPNIRVGYCSQIPNCDMSH-----GDCYRGNGKYM 369  
Db 2728 LRENYCRNPDSGSESPWCTTDPNIRVGYCSQIPNCDMSH-----GDCYRGNGKYM 369  
QY 370 GNLSTQTRSGLTCSMDKNMEDLHRHFWMEPD--ASKLNENYCRNPDDDAHGPMWCTGNP 426  
Db 2787 GNLSTQTRSGLTCSMDKNMEDLHRHFWMEPD--ASKLNENYCRNPDDDAHGPMWCTGNP 426  
QY 427 LIPMDYCPISRCGDTTPT 445

Db 2843 AVRWEYCSIPTCESPTTPT 2861  
Search completed: October 3, 2005, 05:59:59  
Job time: 41.225 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:29 ; Search time 65.3656 Seconds  
(without alignments)  
3501.834 Million cell updates/sec

Title: US-09-674-377B-1

Perfect score: 2604  
Sequence: 1 EKKRRNTLHEFKSAKXTLLI.....IPWDYCPISRCRGDTPTTIV 447

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: uniprot\_03:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2601	99.9	728	1 HGF_HUMAN	P14210 homo sapien
2	2462	94.5	730	2 Q867B7	Q867B7 canis famil
3	2456	94.3	730	2 Q76BS1	Q76BS1 bos taurus
4	2452	94.2	728	2 Q9BH09	Q9BH09 felis silve
5	2409	92.5	728	2 Q8C9G5	Q8C9G5 mus musculu
6	2408	92.5	728	1 HGF_MOUSE	Q08048 mus musculu
7	2401	92.2	728	1 HGF_RAT	P17945 rattus norv
8	2052	78.8	726	2 Q90978	Q90978 gallus gall
9	1864.5	71.6	710	2 Q91402	Q91402 xenopus. he
10	1705.5	65.5	405	2 Q788Q2	Q788Q2 gallus gall
11	1214	46.6	449	2 Q6GR14	Q6GR14 xenopus lae
12	1209.5	46.4	704	2 Q90865	Q90865 gallus gall
13	1208	45.4	716	2 Q91691	Q91691 xenopus lae
14	1180.5	45.3	711	1 HGF_HUMAN	P26927 homo sapien
15	1176	45.2	717	2 P70006	P70006 xenopus lae
16	1172	44.9	709	2 Q90ZK6	Q90ZK6 brachydanio
17	1168.5	44.9	709	2 Q7ZTN8	Q7ZTN8 xenopus lae
18	1163.5	44.7	567	2 Q13Z08	Q13Z08 homo sapien
19	1144	43.9	716	2 P70521	P70521 rattus norv
20	1125	43.2	716	2 HGF_MOUSE	P26928 mus musculu
21	1125	43.2	716	2 Q91XG8	Q91XG8 mus musculu
22	1089	41.8	818	2 Q6PBA6	Q6PBA6 brachydanio
23	1085.5	41.7	832	1 PLMN_RAT	Q01177 rattus norv
24	1080.5	41.5	806	1 PLMN_MOUSE	Q18783 macropus eu
25	1066	40.9	790	2 PLMN_PIG	P06867 sus scrofa
26	1064	40.9	466	2 Q6TC10	Q6TC10 mus musculu
27	1064	40.9	812	1 PLMN_MOUSE	P20918 mus musculu
28	1053.5	40.5	810	1 PLMN_ERIEU	Q29485 erinaceus e
29	1044.5	40.1	810	1 PLMN_MACMU	P12545 macaca mula
30	1042	40.0	810	1 PLMN_HUMAN	P00747 homo sapien
31	1040	39.9	215	2 Q42341	Q42341 gallus gall

32	1038	39.9	812	1 PLMN_BOVIN	P06868 bos taurus
33	1032.5	39.7	759	2 Q7TP84	Q7TP84 rattus norv
34	985	37.8	359	2 Q8MMR1	Q8MMR1 canis famil
35	966.5	37.1	648	2 Q9H1V4	Q9H1V4 homo sapien
36	943.5	36.2	2869	2 Q28398	Q28398 erinaceus e
37	896	34.4	211	2 Q55027	Q55027 mus musculu
38	879	33.8	4548	1 APOA_HUMAN	P08519 homo sapien
39	843.5	32.4	1420	1 APOA_MOUSE	P14417 macaca mula
40	617	23.7	162	2 Q8C4E2	Q8C4E2 mus musculu
41	615	23.6	109	2 Q9N1B8	Q9N1B8 ovis aries
42	444.5	17.1	454	2 Q46506	Q46506 papio hamad
43	439	15.9	75	2 Q9BG99	Q9BG99 bos taurus
44	408.5	15.7	325	1 PLMN_PETUMA	P33574 petromyzon
45	406	15.6	429	2 Q8AVB0	Q8AVB0 brachydanio

## ALIGNMENTS

RESULT 1	ID	HGF_HUMAN	STANDARD	PRT: 728 AA.
AC	P14210	002935	Q13494	Q14519
DT	01-JAN-1990	(Rel. 13, Created)		Q8BCE2; Q9BYU9; Q9BYM0; Q9UDU6;
DT	01-AUG-1991	(Rel. 19, Last sequence update)		
DT	25-OCT-2004	(Rel. 45, Last annotation update)		
DE	Hepatocyte growth factor precursor (Scatter factor) (SF)			
DE	(Hepatopoietin A).			
GN	Name=HGF; Synonyms=HPTA;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	(1)			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	MEDLINE=91340155; PubMed=1831432; DOI=10.1016/0378-1119(91)90080-U;			
RA	Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;			
RT	"Organization of the human hepatocyte growth factor-encoding gene.";			
RL	Gene 102:213-219(1991).			
RN	(2)			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Placenta;			
RX	MEDLINE=89392017; PubMed=2528952;			
RA	Miyazawa K., Tsubouchi H., Naka D., Takahashi K., Okigaki M.,			
RA	Arakaki N., Nakayama H., Hirono S., Sakiyama O., Takahashi K.,			
RT	Gohda E., Daikuhara Y., Kitamura N.;			
RT	"Molecular cloning and sequence analysis of cDNA for human hepatocyte			
RL	growth factor.";			
RL	Biochem. Biophys. Res. Commun. 163:967-973(1989).			
RN	(3)			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Leukocyte;			
RX	MEDLINE=91025062; PubMed=2145836;			
RA	Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa T., Asami O.,			
RA	Hagiya M., Nakamura T., Shimizu S.;			
RT	"Isolation and expression of cDNA for different forms of hepatocyte			
RT	growth factor from human leukocyte.";			
RL	Biochem. Biophys. Res. Commun. 172:321-327(1990).			
RN	(4)			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 55-73 AND 495-520.			
RC	TISSUE=Liver;			
RX	MEDLINE=9006676; PubMed=2511289; DOI=10.1038/342440a0;			
RA	Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimonishi M.,			
RA	Sugimura A., Tashiro K., Shimizu S.;			
RT	"Molecular cloning and expression of human hepatocyte growth factor.";			
RL	Nature 342:440-443(1989).			
RN	(5)			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Placenta;			
RX	MEDLINE=91200041; PubMed=1826653;			
RA	Miyazawa K., Kitamura A., Naka D., Kitamura N.;			
RT	"An alternatively processed mRNA generated from human hepatocyte			
RT	growth factor gene.";			

- RL Eur. J. Biochem. 197;15-22(1991).
- RN [6]
- RA SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 583-592.
- RC TISSUE=lung fibroblast;
- RX PubMed=1824873;
- RA Rubin J.S., Chan A.M.-L., Bottaro D.P., Burgess W.H., Taylor W.G.,
- RA Cech A.C., Hirschfield D.W., Wong J., Miki T., Finch P.W.,
- RA Aaronson S.A.;
- RT "A broad-spectrum human lung fibroblast-derived mitogen is a variant
- RT of hepatocyte growth factor.";
- RL Proc. Natl. Acad. Sci. U.S.A. 88:415-419(1991).
- RN [17]
- RA SEQUENCE FROM N.A. (ISOFORM 1).
- RC TISSUE=embryonic fibroblast;
- RX MEDLINE=91334393; PubMed=1831266;
- RA Weidner K.M., Arakaki N., Hartman G., Vandekerckhove J., Weingart S.,
- RA Riederer H., Fontsch C., Tsubouchi H., Hishida T., Dalkhara Y.,
- RA Birnmeier W.;
- RT "Evidence for the identity of human scatter factor and human
- RT hepatocyte growth factor.";
- RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005(1991).
- RN [18]
- RA SEQUENCE FROM N.A. (ISOFORM 4).
- RX PubMed=1720571;
- RA Chan A.M.-L., Rubin J.S., Bottaro D.P., Hirschfield D.W., Chedid M.,
- RA Aaronson S.A.;
- RT "Identification of a competitive HGF antagonist encoded by an
- RT alternative transcript.";
- RL Science 254:1382-1385(1991).
- RN [19]
- RA SEQUENCE FROM N.A. (ISOFORM 2), AND MUTAGENESIS OF ARG-494.
- RX MEDLINE=93087571; PubMed=1280830;
- RA Hartman G., Naldini L., Weidner K.M., Sachs M., Vigna E.,
- RA Comoglio P.M., Birnmeier W.;
- RT "A functional domain in the heavy chain of scatter factor/hepatocyte
- RT growth factor binds the c-Met receptor and induces cell dissociation
- RT but not mitogenesis.";
- RL Proc. Natl. Acad. Sci. U.S.A. 89:11574-11578(1992).
- RN [110]
- RA SEQUENCE FROM N.A. (ISOFORM 6).
- RX MEDLINE=96278713; PubMed=8662798; DOI=10.1074/jbc.271.22.13110;
- RA Cioce V., Csaky K.G., Chan A.M.-L., Bottaro D.P., Taylor W.G.,
- RA Jensen R., Aaronson S.A., Rubin J.S.;
- RT "Hepatocyte growth factor (HGF)/NK1 is a naturally occurring
- RT HGF/scatter factor variant with partial agonist/antagonist activity.";
- RL J. Biol. Chem. 271:13110-13115(1996).
- RN [111]
- RA SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LYS-304 AND TYR-330.
- RA Riederer H., Livingston R.J., Daniels M.R., Chung M.-W.,
- RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
- RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
- RT "NIHES-SNP, environmental genome project. NIHES ES15478, Department
- RT of Genome Sciences, Seattle, WA (URL: <http://legp.gs.washington.edu>).";
- RL Submitted (FEB-2003) to the EMBL/GenBank/DBD databases.
- RN [121]
- RA SEQUENCE FROM N.A.
- RX MEDLINE=22737099; PubMed=12853948; DOI=10.1038/nature01782;
- RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
- RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
- RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
- RA Fowell G.A., Delenault K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
- RA Van Hout A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
- RA Ozeraky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
- RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
- RA Kozlowski-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
- RA Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Stromatt C.,
- RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
- RA Wendl M.C., Yang S.-P., Schmitt B.R., Wallis J.W., Spielch J.,
- RA Bieri T.R., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,
- RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
- RA Clifton S.W., Chisoe S.U., Marra M.A., Raymond C., Haugen E.,
- RA Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Hubb K.,
- RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
- RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
- RA Bailey J.A., Portnoy M.E., Torrents D., Chirwalla A.T., Gish W.R.,
- RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
- RA Waterston R.H., Wilson R.K.;
- RT "The DNA sequence of human chromosome 7.";
- RL Nature 424:157-164(2003).
- RN [131]
- RA SEQUENCE FROM N.A. (ISOFORMS 5 AND 6).
- RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
- RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
- RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
- RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
- RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
- RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
- RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
- RA Brownstein M.J., Uesli T.B., Toshitsuki S., Cantanti P., Prange C.,
- RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
- RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
- RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
- RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
- RA Fafey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
- RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
- RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
- RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
- RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
- RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
- RT "Generation and initial analysis of more than 15,000 full-length human
- RT and mouse cDNA sequences.";
- RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
- RN [141]
- RA SEQUENCE OF 1-208 AND 249-695 FROM N.A. (ISOFORM 1).
- RX MEDLINE=91369928; PubMed=1832556;
- RA Miyazawa K., Kitamura A., Kitamura N.;
- RT "Structural organization and the transcription initiation site of the
- RT human hepatocyte growth factor gene.";
- RL Biochemistry 30:9170-9176(1991).
- RN [151]
- RA SIGNAL SEQUENCE CLEAVAGE SITE.
- RX MEDLINE=91207365; PubMed=1826837;
- RA Yoshizawa Y., Arakaki N., Naka D., Takahashi K., Hiroo S., Kondo J.,
- RA Nakayama H., Gohda E., Kitamura N., Tsubouchi H., Ishii T.,
- RA Hienida T., Dalkhara Y.;
- RT "Identification of the N-terminal residue of the heavy chain of both
- RT native and recombinant human hepatocyte growth factor.";
- RL Biochem. Biophys. Res. Commun. 175:660-667(1991).
- RN [161]
- RA CARBOHYDRATE-LINKAGE SITE THR-476.
- RX MEDLINE=93129192; PubMed=182348;
- RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
- RA Nakamura T., Shimizu S.;
- RT "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
- RT on the alpha chain.";
- RL Biochem. Biophys. Res. Commun. 189:1329-1335(1992).
- RN [171]
- RA MUTAGENESIS.
- RX MEDLINE=92331602; PubMed=1321034;
- RA Loker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins K.A.,
- RA Baker J.B., Godowski P.J.;
- RT "Structure-function analysis of hepatocyte growth factor:
- RT identification of variants that lack mitogenic activity yet retain
- RT high affinity receptor binding.";
- RL EMBO J. 11:2503-2510(1992).
- RN [181]
- RA STRUCTURE BY NMR OF 31-127.
- RX MEDLINE=9815423; PubMed=9493272; DOI=10.1016/S0969-2126(98)00012-4;
- RA Zhou H., Mazzulla M.J., Kaufman J.D., Stahl S.J., Wingfield P.T.,
- RA Rubin J.S., Bottaro D.P., Byrd R.A.;
- RT "The solution structure of the N-terminal domain of hepatocyte growth
- RT factor reveals a potential heparin-binding site.";
- RL Structure 6:109-116(1998).
- RN [191]
- RA X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.



RA MEDLINE=99036858; PubMed=9817840; DOI=10.1016/S0969-2126(98)00138-5;  
RA Ultsch M., Loker N.A., Godowski P.J., de Vos A.M.;

Query Match 99.9%; Score 2601; DB 1; Length 728;  
Best Local Similarity 99.8%; Pred. No. 1.1e-186;

Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKKRRNTIHEFKSAKTLTIKIDPALKIKTKKNTADQCANRCTRNGKLPFTCKAFVFDK 60  
DB 32 QKKRRNTIHEFKSAKTLTIKIDPALKIKTKKNTADQCANRCTRNGKLPFTCKAFVFDK 91  
QY 61 ARKQCLMPFPNSMSSGVKKEFGHEPDLYENKDIYIRNCIIIGKGSYKGTVSITSGIKCOP 120  
DB 92 ARKQCLMPFPNSMSSGVKKEFGHEPDLYENKDIYIRNCIIIGKGSYKGTVSITSGIKCOP 151  
QY 121 WSMIPIHESFLPSSYRGKDLQENYCRNPRGEGGPMCFNSPEVYEVCDIPQCESEVBC 180  
DB 152 WSMIPIHESFLPSSYRGKDLQENYCRNPRGEGGPMCFNSPEVYEVCDIPQCESEVBC 211  
QY 181 MTCNGESYRGKDLMDHTESGKICQRMHQTPHRRKFLPERYDVKGFDDNYCRNPDGQRPWC 240  
DB 212 MTCNGESYRGKDLMDHTESGKICQRMHQTPHRRKFLPERYDVKGFDDNYCRNPDGQRPWC 271  
QY 241 YTLDPHTRWECYCAIKTCADNTMNDTVPLETTCTCIGQGEGRGTNTTNGIPICORWDS 300  
DB 272 YTLDPHTRWECYCAIKTCADNTMNDTVPLETTCTCIGQGEGRGTNTTNGIPICORWDS 331  
QY 301 OYPHEHDMTPENPKCKDLLENYCRNPDGSESPMCFITTDNIRVGYCSQIPNCDSHGGDC 360  
DB 332 OYPHEHDMTPENPKCKDLLENYCRNPDGSESPMCFITTDNIRVGYCSQIPNCDSHGGDC 391  
QY 361 YGNGKNYMGNLISQTRSGJLTCGSMWCKMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 420  
DB 392 YGNGKNYMGNLISQTRSGJLTCGSMWCKMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 451  
QY 421 CYTGNPLIPWDYCPISRCBGDTTPTTV 447  
DB 452 CYTGNPLIPWDYCPISRCBGDTTPTTV 478  
RESULT 2  
ID 0867B7 PRELIMINARY; PRT; 730 AA.  
AC 0867B7;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)  
DE Hepatocyte growth factor.  
GN Name=hgf;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=Beagle;  
RX MEDLINE=22844761; PubMed=12963274; DOI=10.1016/S0165-2427(03)00118-1;  
RA Miyake M., Saze K., Yaguchi T., Wang J., Suzuta Y., Haga Y.,  
Takashi S.Y., Yamamoto Y., Iwabuchi S.,  
"Canine hepatocyte growth factor: molecular cloning and  
characterization of the recombinant protein.";  
RT Vet. Immunol. Immunopathol. 95:135-143(2003).  
RL (2)  
RP SEQUENCE FROM N.A.  
RA Liao A.T., Chien M.B., London C.A.;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to peptidase family 51.  
DR EMBL; AB090353; BAC57560.1; -;  
DR EMBL; AY543632; AAS48570.1; -;  
DR HSSP; P14210; IGMN.  
DR MEROPS; S01.982; -;  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR011359; HGF\_MST1.  
DR InterPro; IPR000001; Kringle.  
DR InterPro; IPR003014; PAN.  
DR InterPro; IPR003609; Pan\_app.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR Pfam; PF00051; Kringle\_4.  
DR Pfam; PF00024; PAN\_1.  
DR Pfam; PF00089; Trypsin\_1.  
DR PIRSF; PIRSF001152; HGF\_MST1\_1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00018; KRINGLE.  
DR ProDom; PD000395; Kringle\_4.  
DR SMART; SM00473; PAN\_AP\_1.  
DR SMART; SM00020; TRYP\_SPE\_1.  
DR PROSITE; PS00021; KRINGLE\_1\_4.  
DR PROSITE; PS00070; KRINGLE\_2\_4.  
DR PROSITE; PS00948; PAN\_1.  
DR PROSITE; PS0240; TRYPSIN\_DOM\_1.  
KW Hydrolyase, Kringle, Protease, Serine protease.  
SQ SEQUENCE 730 AA; 83398 MW; 4E83F9EABFF6DB1 CRC64;  
Query Match 94.5%; Score 2462; DB 2; Length 730;  
Best Local Similarity 93.1%; Pred. No. 2.9e-176;  
Matches 416; Conservative 19; Mismatches 12; Indels 0; Gaps 0;  
QY 1 EKKRRNTIHEFKSAKTLTIKIDPALKIKTKKNTADQCANRCTRNGKLPFTCKAFVFDK 60  
DB 32 QKKRRNTIHEFKSAKTLTIKIDPALKIKTKKNTADQCANRCTRNGKLPFTCKAFVFDK 91  
QY 61 ARKQCLMPFPNSMSSGVKKEFGHEPDLYENKDIYIRNCIIIGKGSYKGTVSITSGIKCOP 120  
DB 92 ARKQCLMPFPNSMSSGVKKEFGHEPDLYENKDIYIRNCIIIGKGSYKGTVSITSGIKCOP 151  
QY 121 WSMIPIHESFLPSSYRGKDLQENYCRNPRGEGGPMCFNSPEVYEVCDIPQCESEVBC 180  
DB 152 WSMIPIHESFLPSSYRGKDLQENYCRNPRGEGGPMCFNSPEVYEVCDIPQCESEVBC 211  
QY 181 MTCNGESYRGKDLMDHTESGKICQRMHQTPHRRKFLPERYDVKGFDDNYCRNPDGQRPWC 240  
DB 212 MTCNGESYRGKDLMDHTESGKICQRMHQTPHRRKFLPERYDVKGFDDNYCRNPDGQRPWC 271  
QY 241 YTLDPHTRWECYCAIKTCADNTMNDTVPLETTCTCIGQGEGRGTNTTNGIPICORWDS 300  
DB 272 YTLDPHTRWECYCAIKTCADNTMNDTVPLETTCTCIGQGEGRGTNTTNGIPICORWDS 331  
QY 301 OYPHEHDMTPENPKCKDLLENYCRNPDGSESPMCFITTDNIRVGYCSQIPNCDSHGGDC 360  
DB 332 OYPHEHDMTPENPKCKDLLENYCRNPDGSESPMCFITTDNIRVGYCSQIPNCDSHGGDC 391  
QY 361 YGNGKNYMGNLISQTRSGJLTCGSMWCKMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 420  
DB 392 YGNGKNYMGNLISQTRSGJLTCGSMWCKMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 451  
QY 421 CYTGNPLIPWDYCPISRCBGDTTPTTV 447  
DB 452 CYTGNPLIPWDYCPISRCBGDTTPTTV 478  
RESULT 3  
ID 076BS1 PRELIMINARY; PRT; 730 AA.  
AC 076BS1;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)  
DE Hepatocyte growth factor.  
GN Name=hgf;  
OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OC NCBI\_TaxId=9913;  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Yamaji D., Kimura K., Matanabe A., Makondo K., Saito M.,  
 RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL; AB110822; BAD02475.1; -.  
 DR HSP; P08519; IKIV.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR011359; HGF\_MST1.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR003609; Pan\_app.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR Pfam; PF00051; Kringle; 4.  
 DR Pfam; PF00024; PAN; 1.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PIRSF; PIRSF001152; HGF\_MST1; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PD000395; Kringle; 4.  
 DR ProDom; PD000395; Kringle; 4.  
 DR SMART; SM00130; KR; 4.  
 DR SMART; SM00473; PAN\_AP; 1.  
 DR SMART; SM00020; TRYD\_SPC; 1.  
 DR PROSITE; PS00021; KRINGLE\_1; 4.  
 DR PROSITE; PS00070; KRINGLE\_2; 4.  
 DR PROSITE; PS50948; PAN; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR Hydrolase; Kringle; Protease; Serine protease.  
 KW Hydrolyse; 730 AA; 83357 MW; E39D653B0A85F49B CRC64;  
 SQ  
 Query Match 94.3%; Score 2456; DB 2; Length 730;  
 Best Local Similarity 92.6%; Pred. No. 8.2e-176;  
 Matches 414; Conservative 22; Mismatches 11; Indels 0; Gaps 0;

QY 1 EKKRNTTHERFKSAKTLTIKIDPALKIKTKKVTADQCANRCTRNGKLPTCKAFVFDK 60  
 DB 32 QKKRNTTHERFKSAKTLTIKIDPALKIKTKKVTADQCANRCTRNGKLPTCKAFVFDK 91  
 QY 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIGKRSYKGVSTIKSGIKQCP 120  
 DB 92 ARKRCIMFPNMSGGVKKEFGHEFDLYENKDYIRNCIIGKGSYKGVSTIKSGIKQCP 151  
 QY 121 WSSMTPIHESFLPSSYRGKDLQENYCRNRGEGGWCFTSNPEVYEVCDIPQSEVVC 180  
 DB 152 WSSMTPIHESFLPSSYRGKDLQENYCRNRGEGGWCFTSNPEVYEVCDIPQSEVVC 211  
 QY 181 MTCNGESYRGKDLMDHTESGKICQRMHQTPHKKFLUPERYPDGFDDNYCRNPDGQPRPWC 240  
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 QY 241 YLUDPHTRWEYCAIKTCADNTMNDTDLVLETTETCIQGGEGYRGVNTIANGIPCQRWDS 300  
 DB 272 YLUDPHTRWEYCAIKTCADNTMNDTDLVLETTETCIQGGEGYRGVNTIANGIPCQRWDS 331  
 QY 301 QYRPHEDMTPEPKCKDLAEYCRNPDGSESPWCFTTDNINIVGYSQIPNCDSMGQDC 360  
 DB 332 QYRPHEDMTPEPKCKDLAEYCRNPDGSESPWCFTTDNINIVGYSQIPNCDSMGQDC 391  
 QY 361 YGNGKNYVGNLSQTSGLTCSWMDKNMEDLHRHIFWEPDASKLNENYCRNPDGDAHGW 420  
 DB 392 YGNGKNYVGNLSQTSGLTCSWMDKNMEDLHRHIFWEPDASKLNENYCRNPDGDAHGW 451  
 QY 421 CYTGNPLIPMDYCPISRCGEGDTPTTV 447

DB 452 CYTGNPLIPMDYCPISRCGEGDTPTTV 478  
 RESULT 4  
 ID Q9BH09 PRELIMINARY; PRT; 728 AA.  
 AC Q9BH09;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hepatocyte growth factor HGF.  
 GN Name=HGF;  
 OS Fells silvestris cactus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OC NCBI\_TaxId=9685;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Kobayashi Y., Nakamura N., Ishizaka T., Masuda K., Ohno K.,  
 RA Tsujimoto H.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Miyake M., Yaguchi T., Saze K., Suzuta Y., Wang J., Okazaki M.,  
 RA Haga Y., Yamamoto Y., Takahashi S., Iwabuchi S.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL; AB046610; BAB21499.1; -.  
 DR EMBL; AB080187; BAC10545.1; -.  
 DR HSP; P14210; IGMN.  
 DR MEROPS; S01.982; -.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR011359; HGF\_MST1.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR003609; Pan\_app.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR Pfam; PF00051; Kringle; 4.  
 DR Pfam; PF00024; PAN; 1.  
 DR PIRSF; PIRSF001152; HGF\_MST1; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00018; KRINGLE.  
 DR ProDom; PD000395; Kringle; 4.  
 DR SMART; SM00130; KR; 4.  
 DR SMART; SM00473; PAN\_AP; 1.  
 DR SMART; SM00020; TRYD\_SPC; 1.  
 DR PROSITE; PS00021; KRINGLE\_1; 4.  
 DR PROSITE; PS50070; KRINGLE\_2; 4.  
 DR PROSITE; PS50948; PAN; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 KW Hydrolase; Kringle; Protease; Serine protease.  
 SQ SEQUENCE 728 AA; 83067 MW; 8D7F4A333D1E190A CRC64;  
 Query Match 94.2%; Score 2452; DB 2; Length 728;  
 Best Local Similarity 92.6%; Pred. No. 1.6e-175;  
 Matches 414; Conservative 21; Mismatches 12; Indels 0; Gaps 0;

QY 1 EKKRNTTHERFKSAKTLTIKIDPALKIKTKKVTADQCANRCTRNGKLPTCKAFVFDK 60  
 DB 30 QKKRNTTHERFKSAKTLTIKIDPALKIKTKKVTADQCANRCTRNGKLPTCKAFVFDK 89  
 QY 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIGKRSYKGVSTIKSGIKQCP 120  
 DB 90 ARKRCIMFPNMSGGVKKEFGHEFDLYENKDYIRNCIIGKGSYKGVSTIKSGIKQCP 149  
 QY 121 WSSMTPIHESFLPSSYRGKDLQENYCRNRGEGGWCFTSNPEVYEVCDIPQSEVVC 180

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Db 150 MNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCFPTSNBEVREYECDDIQCESEVBC
Qy 181 MTCNGESYRGLMDHTESGKICQRMWDQTPRRHKFLPERYDCKGFDDNYCGRNPDGQRPWC
Db 210 MTCNGESYRGLMDHTESGKICQRMWDQTPRRHKFLPERYDCKGFDDNYCGRNPDGQRPWC
Qy 241 YTLDPRTREYCAIKTCADNTMNDTVPLETTETCICQOGEYRGVTIWNIGIPCRQWMS
Db 270 YTLDPRTREYCAIKTCADNTMNDTVPLETTETCICQOGEYRGVTIWNIGIPCRQWMS
Qy 301 QYPHEDMTPEPKCKCDLRNRYCRNPDGSGSPWCFTTDPNIRYGCQIIPNCMSHGQDC
Db 330 QYPHOHDTPEPKCKCDLRNRYCRNPDGSGSPWCFTTDPNIRYGCQIIPNCMSHGQDC
Qy 361 YRGNKGYMGNLSQTRSGLTCSMWDMKMDLHHIFWEPPASKLNNYCRNPDGDAHGPW
Db 390 YRGNKGYMGNLSQTRSGLTCSMWDMKMDLHHIFWEPPASKLNNYCRNPDGDAHGPW
Qy 421 CYTGNPLIPWDYCPISRCBGDTTPTIV 447
Db 450 CYTGNPLIPWDYCPISRCBGDTTPTIV 476

RESULT 5
ID Q8C9G5 PRELIMINARY; PRT; 728 AA.
AC Q8C9G5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone: A630060C16 product: hepatocyte growth factor, full
DE insert sequence.
OS Name:Hgf;
OC Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RT Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RT Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RT RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The PANTOM Consortium;
RT The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RT Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RT Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
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RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunai T., Taahito H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishize T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RT Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahita S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR HSBP; AK042121; BAC31175.1; -.
DR MGD; MGI:96079; Hgf.
DR GO; GO:0008283; P:cell proliferation; IDA.
DR GO; GO:0008282; P:cellular morphogenesis; IDA.
DR InterPro: IPR011359; HGF_MST1.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001152; HGF_MST1; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRODOM; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS00070; KRINGLE_2; 4.
DR PROSITE; PS00948; PAN; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 728 AA; 82990 MW; 8D5258DF3BCF3545 CRC64;

Query Match 92.5%; Score 2409; DB 2; Length 728;
Best local Similarity 91.1%; Pred. No. 2,7e-172;
Matches 407; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

Qy 1 EKKRRNTLHEPKKSAKTLTIKIDPALKIITKRVNTADQCANRCTRNGSLPTCKAFVFDK
Db 33 OKRRNTLHEPKKSAKTLTIKIDPALKIITKRVNTADQCANRCTRNGSLPTCKAFVFDK
Qy 61 ARKQCLMPFPNMSGVKKFEGHEDLVENKYYINRCITIGKRSYKGTYSITKSGIKKCP
Db 93 SRKRCWVPNMSGVKKFEGHEDLVENKYYINRCITIGKRSYKGTYSITKSGIKKCP
Qy 121 MNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCFPTSNBEVREYECDDIQCESEVBC
Db 153 MNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCFPTSNBEVREYECDDIQCESEVBC
Qy 181 MTCNGESYRGLMDHTESGKICQRMWDQTPRRHKFLPERYDCKGFDDNYCGRNPDGQRPWC
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Db 213 MTCNSESVRGPMHDTESGKTCQRMDOQTPEHRHKFLPERKPDGKFPDNNCRNPDGKPRPMC 272  
Oy 241 YTLDDHTWMEVCAITTCADNTMNDVDVPLETTECTIOGEGRGVNTIMNGICPORRDS 300  
Db 273 YTLDDHTWMEVCAITTCASAVNETDVPETTECTIOGEGRGVNTIMNGICPORRDS 332  
Oy 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCTTDPNIRVGCSOI PNCDMSHGQDC 360  
Db 333 QYPHGHDTTPENFKCKDLRENYCRNPDGSESPWCTTDPNIRVGCSOI PNCDVSSGQDC 392  
Oy 361 YRGNKNYMGNISQTRSGITCSMDKNMEDLHRHIFWEPDASKNENYCRNPDGDAHPW 420  
Db 393 YRGNKNYMGNISKTRSGITCSMDKNMEDLHRHIFWEPDASKNKNYCRNPDGDAHPW 452  
Oy 421 CYTGNPLIPMDYCPISRCGGDTTPITV 447  
Db 453 CYTGNPLIPMDYCPISRCGGDTTPITV 479

## RESULT 6

HGF\_MOUSE STANDARD; PRT; 728 AA.

AC Q08048; Q61662; Q64007;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Hepatocyte growth factor precursor (Scatter factor) (SF)  
DE (Hepatopoietin A).  
GN Name=Hgf;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND SEQUENCE OF 496-504.  
RC TISSUE=Mammary fibroblast;  
RX MEDLINE=9418357; PubMed=815822;  
RA Sasaki M., Nishio M., Sasaki T., Enami J.;  
RT "Identification of mouse mammary fibroblast-derived mammary growth  
RT factor as hepatocyte growth factor";  
RL Biochem. Biophys. Res. Commun. 199; 772-779 (1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=9436381; PubMed=8081873;  
RA Lee C.C., Kozak C.A., Yamada K.M.;  
RT "Structure, genetic mapping, and expression of the mouse Hgf/scatter  
RT factor gene";  
RL Cell Adhes. Commun. 1; 101-111 (1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=94060105; PubMed=8241272; DOI=10.1016/0167-4781(93)90159-B;  
RA Liu Y., Michalopoulos G.K., Zarnegar R.;  
RT "Molecular cloning and characterization of cDNA encoding mouse  
RT hepatocyte growth factor";  
RL Biochim. Biophys. Acta 1216; 299-303 (1993).  
CC -I- FUNCTION: HGF is a potent mitogen for mature parenchymal  
CC hepatocyte cells, seems to be an hepatotrophic factor, and acts as  
CC growth factor for a broad spectrum of tissues and cell types. It  
CC has no detectable protease activity.  
CC -I- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a  
CC disulfide bond.  
CC -I- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Long;  
CC IsoId=Q08048-1; Sequence=Displayed;  
CC Name=Short;  
CC IsoId=Q08048-2; Sequence=VSP\_005408;  
CC -I- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen  
CC subfamily.  
CC -I- SIMILARITY: Contains 4 kringle domains.

CC -I- SIMILARITY: Contains 1 PAN domain.

CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; D10212; BAA01064.1; -;  
DR EMBL; D10213; BAA01065.1; -;  
DR EMBL; S71816; AAB31855.1; -;  
DR EMBL; X72307; CAAS1054.1; ALT\_INIT.  
DR PIR; JC2117; A60185.  
DR HSSP; P14210; 1BHT.  
DR MEROPS; S01.982; -;  
DR MGD; MGI:96079; Hgf.  
DR GO; GO:0008283; P:cell proliferation; IDA.  
DR GO; GO:000902; P:cellular morphogenesis; IDA.  
DR InterPro; IPR000001; Kringle.  
DR InterPro; IPR003014; PAN.  
DR InterPro; IPR003609; Pan\_app.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00051; Kringle; 4.  
DR Pfam; PF00024; PAN; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR PIRSF; PIRSF001152; HGF\_MST1; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00018; KRINGLE.  
DR ProDom; PD000395; Kringle; 4.  
DR SMART; SMO0130; KR; 4.  
DR SMART; SMO0473; PAN\_AP; 1.  
DR SMART; SMO0020; TRYP\_Spec; 1.  
DR PROSITE; PS00021; KRINGLE\_1; 4.  
DR PROSITE; PS50070; KRINGLE\_2; 4.  
DR PROSITE; PS50948; PAN; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
KW Alternative splicing; Direct protein sequencing; Glycoprotein;  
KW Growth factor; Kringle; Pyroglutamate carboxylic acid; Repeat;  
KW Serine protease homology; Signal.  
FT SIGNAL 1 32  
FT CHAIN 33 495  
FT CHAIN 496 728  
FT MOD\_RES 33 33  
FT DOMAIN 38 124  
FT DOMAIN 129 207  
FT DOMAIN 212 289  
FT DOMAIN 306 384  
FT DOMAIN 392 470  
FT DOMAIN 496 728  
FT DISULFID 71 97  
FT DISULFID 75 85  
FT DISULFID 488 607  
FT CARBOHYD 295 295  
FT CARBOHYD 403 403  
FT CARBOHYD 569 569  
FT CARBOHYD 656 656  
FT VARSPPLIC 163 167  
FT CONFLICT 344 344  
FT CONFLICT 479 479  
FT CONFLICT 564 564  
SQ SEQUENCE 728 AA; 82944 MW; A0381FC497534328 CRC64;

Query Match 92.5%; Score 2408; DB 1; Length 728;

Best Local Similarity 91.1%; Pred. No. 3, 2e-172;  
Matches 407; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ERKRRTIHEPKSAKTLIKIPALIKIKYKVVNTADQCANRCRTRNKGLPFTCAAFVFDK 60

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Db 33 OKRRNTLHEPKKSAKTLTKEDPLKIKTKKVNNSADECANRCIRNKGFTPTCKAFVFDK 92
Qy 61 ARKOCIMPFPPNMSGVKKFEGHEPDLVKNKYIRNCIIIGKGRSYGTVSITKSGIKCOP 120
Db 93 SKRCYWPFPNMSGVKKFGHEPDLVKNKYIRNCIIIGKGSYKGTVSITKSGIKCOP 152
Qy 121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCESEVC 180
Db 153 WMSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCESEVC 212
Qy 181 MTCNGESTYGLMDHTBESGKICORMDHQTHRKFLPERYPDYGFDDNVCNRPDDGQPRMC 240
Db 213 MTCNGESTYRGPMHTBESGKICORMDQTPHRAKFLPERYPDYGFDDNVCNRPDDGQPRMC 272
Qy 241 YTLDDHTREVCATKTCANNTMNDVPLETTECTOCGEGYRGTVNTIWNIGPCORRMS 300
Db 273 YTLDDHTREVCATKTCANNTMNDVPLETTECTOCGEGYRGTVNTIWNIGPCORRMS 332
Qy 301 QYRHEHDMTPENFKCKDLRENYCRNPDGSESPWCTTDDNINRGYCSQIPNCDMSHGDC 360
Db 333 QYRPHHDTIPENFKCKDLRENYCRNPDGSESPWCTTDDNINRGYCSQIPKCDVSSGDC 392
Qy 361 YRGNKNYWGNTLSQTRSGITCSMMDXNMDLHRHIFWEPDASKLNNYCRNPDGDAHGW 420
Db 393 YRGNKNYWGNTLSQTRSGITCSMMDXNMDLHRHIFWEPDASKLNNYCRNPDGDAHGW 452
Qy 421 CYTGNPLIPMDYCPISRCGSDTPTTV 447
Db 453 CYTGNPLIPMDYCPISRCGSDTPTTV 479

RESULT 7
HGF_RAT STANDARD; PRT; 728 AA.
ID HGF_RAT STANDARD; PRT; 728 AA.
AC PI7945;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hepatocyte growth factor precursor (Scatter factor) (Sf)
DE (Hepatopoietin A).
GN Name=Hgf;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=90222197; PubMed=2139229;
RA Toshiro K., Hagiya M., Nishizawa T., Seki T., Shimonishi M.,
RA Shimizu S., Nakamura T.,
RT "Deduced primary structure of rat hepatocyte growth factor and
RT expression of the mRNA in rat tissues.";
RN Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=91031482; PubMed=2146117;
RA Okajima A., Miyazawa K., Kitamura N.,
RT "Primary structure of rat hepatocyte growth factor and induction of
RT its mRNA during liver regeneration following hepatic injury.";
RN Eur. J. Biochem. 193:375-381(1990).
CC -!- FUNCTION: HGF is a potent mitogen for mature parenchymal
CC hepatocyte cells, seems to be an hepatotrophic factor, and acts as
CC growth factor for a broad spectrum of tissues and cell types. It
CC has no detectable protease activity.
CC -!- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
CC disulfide bond.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC subfamily.
CC -!- SIMILARITY: Contains 4 kringle domains.
CC -!- SIMILARITY: Contains 1 PAN domain.
```

```
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CC or send an email to license@isb.ch).
CC -----
Db 1 EKRRTNTHPEPKKSAKTLTKEDPLKIKTKKVNNSADECANRCIRNKGFTPTCKAFVFDK 60
Qy 33 OKRRNTLHEPKKSAKTLTKEDPLKIKTKKVNNSADECANRCIRNKGFTPTCKAFVFDK 92
Db 61 ARKOCIMPFPPNMSGVKKFEGHEPDLVKNKYIRNCIIIGKGRSYGTVSITKSGIKCOP 120
Qy 93 SKRCYWPFPNMSGVKKFGHEPDLVKNKYIRNCIIIGKGSYKGTVSITKSGIKCOP 152
Db 121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCESEVC 180
Qy 153 WMSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCESEVC 212
Db 181 MTCNGESTYGLMDHTBESGKICORMDHQTHRKFLPERYPDYGFDDNVCNRPDDGQPRMC 240
Qy 213 MTCNGESTYRGPMHTBESGKICORMDQTPHRAKFLPERYPDYGFDDNVCNRPDDGQPRMC 272
Db 241 YTLDDHTREVCATKTCANNTMNDVPLETTECTOCGEGYRGTVNTIWNIGPCORRMS 300
Qy 273 YTLDDHTREVCATKTCANNTMNDVPLETTECTOCGEGYRGTVNTIWNIGPCORRMS 332
Db 301 QYRHEHDMTPENFKCKDLRENYCRNPDGSESPWCTTDDNINRGYCSQIPNCDMSHGDC 360
Qy 333 QYRPHHDTIPENFKCKDLRENYCRNPDGSESPWCTTDDNINRGYCSQIPKCDVSSGDC 392
Db 361 YRGNKNYWGNTLSQTRSGITCSMMDXNMDLHRHIFWEPDASKLNNYCRNPDGDAHGW 420
Qy 393 YRGNKNYWGNTLSQTRSGITCSMMDXNMDLHRHIFWEPDASKLNNYCRNPDGDAHGW 452
Db 421 CYTGNPLIPMDYCPISRCGSDTPTTV 447
Qy 453 CYTGNPLIPMDYCPISRCGSDTPTTV 479

Query Match 92.2%; Score 2401; DB 1; Length 728;
Best Local Similarity 90.4%; Pred. No. 1.1e-171;
Matches 404; Conservative 23; Mismatches 20; Indels 0; Gaps 0;
Qy 1 EKRRTNTHPEPKKSAKTLTKEDPLKIKTKKVNNSADECANRCIRNKGFTPTCKAFVFDK 60
Db 33 OKRRNTLHEPKKSAKTLTKEDPLKIKTKKVNNSADECANRCIRNKGFTPTCKAFVFDK 92
Qy 61 ARKOCIMPFPPNMSGVKKFEGHEPDLVKNKYIRNCIIIGKGRSYGTVSITKSGIKCOP 120
Db 93 SKRCYWPFPNMSGVKKFGHEPDLVKNKYIRNCIIIGKGSYKGTVSITKSGIKCOP 152
Qy 121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCESEVC 180
Db 153 WMSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCESEVC 212
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QY	161	MTMCNESYXGLADHTHESGKLCQRMHOTHYRHRKFLBERYPDKGFDNNYCRNPDGQRRPWC	2410
Db	213	MTMCNESYXGPMDDHTESGKTCQRMDOQTPIRHRFLBERYPDKGFDNNYCRNPDGKRRPWC	2722
QY	241	YTLDEHTRWYCAIKTCADNTMNDTVPLETTECIGQGGEGYRGTVNTIWNIGLIPCORWDS	3000
Db	273	YTLDEPDTPEWYCAIKKCAHSAVNETDVPMETTECIGQGGEGYRGTNTIWNIGLIPCORWDS	3322
QY	301	QYPRHEHDMTPENPKCDLRENYCRNNDGSSSPKCFITTDPIRIRYGSQIIPNCMSHGDC	3600
Db	333	QYPRHKDITIPENPKCDLRENYCRNPDGASPPKCFITTDPIRIRYGSQIIPKCVSSQDC	3922
QY	361	YRGNKNYVGNLSQTRSGLTCSMWDMKMDLJHHIEMEPDASKLENENYCRNPDDAHGPW	4200
Db	393	YRGNKNYVGNLSKTRSGLTCSMWDMKMDLJHHIEMEPDASKLTKNYCRNPDDAHGPW	4522
QY	421	CYTGNDPLMPDYCPISRCEGDTTPIIV	447
Db	453	CYTGNDPLMPDYCPISRCEGDTTPIIV	479

## RESULT 8

ID	Q90978	PRELIMINARY;	PRF;	726 AA.
AC	Q90978	Q90866;		
DT	01-JAN-1998	(TREMBLrel. 05, Created)		
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	Hepatocyte growth factor / scatter factor.			
GN	Name=HGF/SF;			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauirata; Aves; Neognathae; Galliformes; Psittacidae; Psittacinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96029010; PubMed=7554499;			
RA	They C., Sharpe M.J., Bailey S.D., Stern C.D., Gherardi E.;			
RT	"Expression of HGF/SF, HGF/MSP and c-met suggests new functions			
RT	during early chick development.";			
RL	Dev. Genet. 17:90-101(1995).			
CC	-1- SIMILARITY: Belongs to peptidase family S1.			

DR HSS

DR GO; GO:0004233, F:chymotrypsin activity, IEA.  
DR GO; GO:0004233, F:peptidase activity, IEA.  
DR GO; GO:0004295, F:trypsin activity, IEA.  
DR GO; GO:0006508, P:proteolysis and peptidolysis, IEA.  
DR Pfam; PF00051, Kringle\_4.  
DR Pfam; PF00024, PAN; 1.  
DR Pfam; PF00089, Trypsin; 1.  
DR PfamSF; PfamSF00152, HGF\_MST1; 1.  
DR PRINTS; PR00722, CHMOTRYPSIN.  
DR PRINTS; PR0018, KRINGLE.  
DR ProDom; PD000395, Kringle; 4.  
DR SMART; SM00130, KR; 4.  
DR SMART; SM00473, PAN AP; 1.  
DR SMART; SM00020, Tryp\_SPC; 1.  
DR PROSITE; PS00021, KRINGLE\_1; 4.  
DR PROSITE; PS00070, KRINGLE\_2; 4.  
DR PROSITE; PS00948, PAN; 1.  
DR PROSITE; PS0240, TRYPSIN\_DOM; 1.  
DR HydroLase; Kringle; Protease; Serine protease.  
KW SEQUENCE 726 AA; 8265 MW; 5BD06CFB5C40B003 CRC64;

Query Match

Best Local Similarity 76.6%; Pred. No. 1.6e-145;

Matches 341; Conservative 49; Mismatches 53; Indels 2; Gaps 1,

Qy 3 KRRTTIEEFKSAKTTLLKIDPALAKIKTKYKNTADOCANCRTRNKGIPFTCAFVEDKAR 62

Db	30	XRBNPLHYYKKTGELMLKANKTLEBVKTKLNTTBOCARCGRNKGSLSTCCAFADRYT	69
Qy	63	KQCLMFPPNSMSSGVYKEFGEFDLYENKDYIRNCIIGKGRSYKGTVSTTKSGIKQCPMS	122
Db	90	KRCHLSNLSLNTNGRKQKHDFDLFEKKDYARNCCIIGKAGAYKGTISITKSGIOCCAWN	149
Qy	123	SMIPIHEHFLSSVYKGDLOEYCNCPNGEEGPMCFNSPEVRYEVCIPQSEVEECMT	182
Db	150	SMIPIHEHFLSSVYKGDIRENYCNPREEBGPWCFTTSPQMRHEVCIPQSEVEECMT	209
Qy	183	CNGESYRSRLMDHTSESGKICQRMWDHOTPHRKFLPERYPDKGFDVDVNCRNPDGQPRDWCYT	242
Db	210	CNGESYRCPMDHTSESGEQQRMDLQRPHKHKRPREYRPDKGFDVDVNCRNPDGKRLRWCYT	269
Qy	243	LDPRTRWEYCAIKTCADNTMNDTVPLETTECIQCGEGYRGTVNTINAGIPQQRDSDQY	302
Db	270	LDPRTPMEFCAIKTCDDVGLNSTEVAELTTTCIOGQEGEYRGTVNTIWSGICQQRMDSDP	329
Qy	303	PHEHMTPEENFPCXDLRENYCNPAPGSESPWCFTTDPNIRVYCSQIPIQCDSMHGDDCYR	362
Db	330	PHQNHITPEENFCXDLRENYCNPAPGSESPWCFTTDPNIRIGCSQIPIQCDVSNEDCYR	389
Qy	363	GNKKNYMGNLISOTRSGLTCSMMDKMDMEDLHRH--ITFWEADASKLNEYNCRNPPDDAHGPW	420
Db	390	GNKGSYMGNLISNTRIGLTCSITWCKDNIEDLRRIHQIFREBDVSKLKNKYCRNPDDDPHGPW	449
Qy	421	CYTGNPPLIPWDYCPISRCBGDTTPT	445
Db	450	CYTDPLIPWDYCPISRCTGDTTPT	474

## RESULT 9

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ID 091402 PRELIMINARY; PRT; 710 AA.
AC O91402;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hepatocyte growth factor.
GN Name=HGF;
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae
OX NCBI_taxid=8353;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tailbud;
RX MEDLINE=55267660; PubMed=7748783; DOI=10.1016/0925-4773(94)00309-B;
RA Nakamura H., Teshiro K., Nakamura T., Shikawa K.;
RT "Molecular Cloning of Xenopus HGF cDNA and its expression studies in
RT Xenopus early embryogenesis."
RL Mech. Dev. 49:123-131(1995).
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; S77422; AAB34354.2; -.
DR HSSP; P14210; IGMN.
DR MEROPS; S01.976; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001152; HGF_MST1; 1.
DR PRINTS; PR00722; CHYMOTRYPIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PSS0070; KRINGLE_2; 4.

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RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzyzanski M.I., Skalski U., Smalls D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.,  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative.";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Klein S., Strausberg R.,  
 RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.  
 DR EMBL, BC073334; AAH73334.1; -;  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0003809; F:thrombin activity; IEA.  
 DR GO; GO:0007596; P:blood coagulation; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR003609; Pan\_app.  
 DR InterPro; IPR003966; Peptidase\_S1A\_pr.  
 DR Pfam; PF00024; Kring1; 4.  
 DR Pfam; PF00024; PAN; 1.  
 DR PRINTS; PR00018; KRINGLE.  
 DR PRODOM; PD000395; PROTHROMBIN.  
 DR SMART; SM00130; KR; 4.  
 DR SMART; SM00473; PAN\_AP; 1.  
 DR PROSITE; PS00021; KRINGLE\_1; 4.  
 DR PROSITE; PS50070; KRINGLE\_2; 4.  
 DR PROSITE; PS50948; PAN; 1.  
 KW Kring1.  
 SQ SEQUENCE 449 AA; 52467 MW; 5C2CE4B708E13D0B CRC64;

Query Match 46.6%; Score 1214; DB 2; Length 449;  
 Best Local Similarity 47.3%; Pred. No. 6; 8e-83;  
 Matches 207; Conservative 74; Mismatches 145; Indels 12; Gaps 6;

OY 5 RNTIHEFKSAATTLIKIDPALIKITKKNVTADQCANRCTRNGKLPFTCKAFVFDKARQ 64  
 DB 21 RSLNDYQKSGKLELVHMNG-GVKQEIQSEIQVCAKQCS-LLDCRSFVYMWKSGS 75  
 OY 65 CLMFPPNMSGVKKFEGHEFDLYENKDIYINCIIGKRSYKGVTSITSGIKCQPMWSM 124  
 DB 76 CLLEPTONSANVLLQRNVOYDLQKQDYIRCCVANGTGYTGYSKTSKGTCCRRWLK 135  
 OY 125 IPHESFLPSSYRGKDLQENYCRNPGEEGPWCFTSNPEYRYEVDIPQCESEVCMTCN 184  
 DB 136 FPHDKFSPITW--PUEENYCRNPDSDEGPMWCTTIDKNIRHGYGICKCEDAVCLTIN 193  
 OY 165 GESYGLMDHTESGKICQRMWHQTPHRAKFLPERYPDKGFDNDYCRNPDGQRPWCYTLD 244  
 DB 194 GSDYGSVDRTEGSKQCRWDLQTPHAHPYKPEKYPDKSLDNDYCRNPSSSRPWCYTLD 253  
 OY 245 PHTREYCAIKTCADNTMDTVPLETTTCIOGGGSGYGVYTWINGIPCCQRMDSQYH 304  
 DB 254 PAVEKEFCITKCKQKRLSNIET--TSYCFKREGSGYKANTTSTSGIPCCQRMDSQYH 310  
 OY 305 EHDMTPENFCKDLRENYCRNPDSGSPMCFCTTDPIRIVGYCSQIPNC-DMGHGDDCYRG 363  
 DB 311 SHRFLEPKYPCAGLDENYCRNPDSGSPMCFCTTLPGRMAVYCFQIKKCDVLEPDCYHG 370

OY 364 NGKNYMGULSOTRSLGTSMDKNNEDLHRIIFWEPPDASKINENYCRNPDDAHGPMCT 423  
 DB 371 NGELISGVRGSTRKIKRMRWEKRNLDLESLD-QPYLVPUEENYCRNPDRDSHGPMCT 429  
 OY 424 GNPLIPMDYCPISRCESD 441  
 DB 430 MDNTPFDYCAIKPCEGE 447

RESULT 12  
 ID 090855 PRELIMINARY; PRT; 704 AA.  
 AC 090855;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Hepatocyte growth factor-like/macrophage stimulating protein.  
 GN Name=HGF/MSP;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=96029010; PubMed=7554499;  
 RA Thery C., Sharpe M.J., Batley S.J., Stern C.D., Gherardi E.;  
 RT "Expression of HGF/SF, HGF/MSP and c-met suggests new functions  
 RT during early chick development.";  
 RL Dev. Genet. 17:90-101(1995).  
 CC -i SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL, X80433; CAA58862.1; -;  
 DR HSSP; P00747; ICEA.  
 DR MEROPS; S01.977; -;  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR Pfam; PF00051; Kring1; 4.  
 DR Pfam; PF00024; PAN; 1.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PIRSF; PIRSF001152; HGF\_MST1; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRODOM; PD000395; Kring1; 4.  
 DR SMART; SM00130; KR; 4.  
 DR SMART; SM00473; PAN\_AP; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00021; KRINGLE\_1; 4.  
 DR PROSITE; PS50070; KRINGLE\_2; 4.  
 DR PROSITE; PS50948; PAN; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 KW Hydrolyase; Kring1; Protease; Serine protease.  
 SQ SEQUENCE 704 AA; 79341 MW; CAB0D8C41367C37 CRC64;

Query Match 46.4%; Score 1209.5; DB 2; Length 704;  
 Best Local Similarity 46.0%; Pred. No. 2; 4e-82;  
 Matches 207; Conservative 71; Mismatches 149; Indels 23; Gaps 8;

OY 5 RNTIHEFKSAATTLIKIDPALIKITKKNVTADQCANRCTRNGKLPFTCKAFVFDKARQ 64  
 DB 20 RSLNDFORLGTETELRAAPNEPPSAPAHGAQCAQCANRP--DCRAFHHEROSL 75  
 OY 65 CLMFPPNMSGVKKFEGHEFDLYENKDIYINCIIGKRSYKGVTSITSGIKCQPMWSM 124  
 DB 76 CQLLPWSQSRSPEARLQKNIHYDLQKDFLBCIVANGSTRGTRDITTEGRGRCWHQAT 135  
 OY 125 IPHESFLPSSYRGKDLQENYCRNPGEEGPWCFTSNPEYRYEVDIPQCESEVCMTCN 184  
 DB 136 TPHDRFLPSLRNG--LEENYCRNPDRDKGPMWCTTVDPNVRHQSGLIKKCEDAVCMTCN 193  
 OY 165 GESYGLMDHTESGKICQRMWHQTPHRAKFLPERYPDKGFDNDYCRNPDGQRPWCYTLD 244



Db 194 GEDYRFEVHTESGTECORWDLQHPKHHPDPKYEKGJLDNDYCNPNSSSEPCWCTYTD 253  
QY 245 PHTRWEYCAIKTCADNTMNDVPLR-ETTEICGSGEGYRGVNTIWMGIPCORWDSOYR 303  
Db 254 PALERFECIRYVKRPR-----PIVTTTCIRGKEGEGRGRRNVTVSGIPCORWDAQTL 308  
QY 304 HEHDMTPENFKCDLRENYCRNPDGSESPWCFTTDNIRVGYCSQIPNCDSM-HGQDCYR 362  
Db 309 HRHFPVSPKPCKDLOENYCRNPDGSEBAPWCFTTRGMRVAFCFHTRCDDDELDAECVH 368  
QY 363 GNGKATYMGULSOTRSGLTCSMDKXNMDLHRH1-----FWEPDASKLNEYCNRPDDAH 417  
Db 369 GHGERYHGHVSKTRKGIICORWDATTP---HYPOISPTTHPEA-HLEKNYCRNPDNDSH 423  
QY 418 GPMCTGNPLIPWDYCPISRCBGDTTPTI 447  
Db 424 GPMCTGNPLIPWDYCPISRCBGDTTPTI 453

## RESULT 13

091691 PRELIMINARY; PRT; 716 AA.  
AC 091691;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)  
DE Growth factor Liverline.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ruiz i Altaba A., Thery C.;  
RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U57455; AAB52574.1; -  
DR HSSP; P00746; 1FDP.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0003809; F:thrombin activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0007596; P:blood coagulation; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR Pfam; PF00051; Kringle; 4.  
DR Pfam; PF00024; PAN; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR PIRSF; PIRSF001152; HGF\_MST1; 1.  
DR PRINTS; PRO0722; CHYMOTRYPSIN.  
DR PRINTS; PRO0018; KRINGLE.  
DR PRINTS; PRO1505; PROTHROMBIN.  
DR ProDom; PD000395; Kringle; 4.  
DR SMART; SM00130; KR; 4.  
DR SMART; SM00473; PAN\_A; 1.  
DR SMART; SM00020; TRYD\_SPC; 1.  
DR PROSITE; PS00021; KRINGLE\_1; 4.  
DR PROSITE; PS50948; KRINGLE\_2; 4.  
DR PROSITE; PS50948; PAN; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR Hydrolase; Kringle; Protease; Serine protease.  
SQ SEQUENCE 716 AA; 81971 MW; 508376A0E4398798 CRC64;

## Query Match

Best Local Similarity 46.4%; Score 1208; DB 2; Length 716;  
Matches 207; Conservative 75; Mismatches 149; Indels 12; Gaps 6;

QY 5 RNTIHEFKSAATTLIKITKATNTADOCANRCTRNKGLPFTCAKAFVFKARQ 64  
Db 31 RSLANDYQSKGLIELVHANNNG-GVKEIOSEIQVCAKQCS-----LLDCRSFYVMNKSQT 85  
QY 65 CLMFPPNMSGGVKGFEHGFDELLENKDYIRNCTICKGRSYKGTVSITYSGIKCOPWSM 124

Db 86 CELLPWTONSANVLLQNRVQYDLYOKKDYIRDCVANGNTYRGTVSKTSKGRTCORWRLK 145  
QY 125 IHEHSFLUSSYRGKDLQENYCRNPDGSEGMWCFSTNSPEVAYEVDIPQSGEVECMCN 184  
Db 146 FPHDKHFSFIHW--BELEENYCRNPDSDPEGMWCTTDDKNINHOYCGIKCKEDAVCLCN 203  
QY 185 GESYGLMDHTESGKICQRMHDQTPHRHKLPERYPDKGFDDNYCRNPDGQPRPWCTYTD 244  
Db 204 GEDYGSVDRTESSGKECQWDLQTPAHYKREKIPDKSLDNDYCRNPDSSSRPWCTYTD 263  
QY 245 PHTRWEYCAIKTCADNTMNDVPLR-ETTEICGSGEGYRGVNTIWMGIPCORWDSOYR 304  
Db 264 PVEKEBFECITCKCKQRLSNIEI---TSTCFKEREGEGYRGKANTTSGIPCORWDSQTPQ 320  
QY 305 EHDMTPENFCKCDLRENYCRNPDGSESPWCFTTDNIRVGYCSQIPNC-DMSGQDCYR 363  
Db 321 SHRFLPEKYPCKGLDENYCRNPDGSEBAPWCFTTLGMRNAYCFQIKCKDVLLEPDCYH 380  
QY 364 NGKNYMGULSOTRSGLTCSMDKXNMDLHRH1FWEPDASKLNEYCNRPDDAHGPMCT 423  
Db 381 NGELYSGRVSKTRKGIKCRMEKXNDLESLD-QYLVPLLEENYCRNPDNRSDHPWCT 439  
QY 424 GNPILIPWDYCPISRCBGDTTPTI 446  
Db 440 MDPNTPFDYCAIKPCEGEKVTL 462

## RESULT 14

HGFL\_HUMAN STANDARD; PRT; 711 AA.  
ID HGFL\_HUMAN

AC P26927; Q13350; Q14870;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, last sequence update)  
DT 25-OCT-2004 (Rel. 45, last annotation update)  
DE Hepatocyte growth factor-like protein precursor (Macrophage stimulatory protein) (MSP) (Macrophage stimulating protein).  
GN Name=MST1; Synonyms=HGFL, Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RX MEDLINE=92002016; PubMed=1655021;  
RA Han S., Stuart L.A., Friesner Degen S.J.;  
RT Identification of the DNF152 locus on human chromosome 3;  
RT to hepatocyte growth factor.";  
RL Biochemistry 30:9768-9780(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=93340141; PubMed=8393443;  
RA Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;  
RT "Cloning, sequencing, and expression of human macrophage stimulating protein (MSP, MST1) confirms MSP as a member of the family of kringle proteins and locates the MSP gene on chromosome 3.";  
RL J. Biol. Chem. 268:15461-15468(1993).  
RN [3]  
RP SEQUENCE OF 230-247; 288-310; 326-341; 484-501; 530-549; 574-596 AND  
RP 602-611, AND SUBUNIT.  
RC TISSUE=Plasma;  
RX PubMed=1827141;  
RA Skeel A., Yoshimura T., Showalter S.D., Tanaka S., Appella E., Leonard E.J.;  
RT "Macrophage stimulating protein: purification, partial amino acid sequence, and cellular activity".  
RL J. Exp. Med. 173:1227-1234(1991).  
CC -!- FUNCTION: Probably has no proteolytic activity, since crucial AA characteristic of serine proteases catalytic sites are not conserved.

CC -1- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a  
 CC disulfide bond.  
 CC -1- PTM: May be cleaved after Arg-483, to yield two chains held  
 CC together by disulfide bonds, or two separate polypeptides.  
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 1 kringle domains.  
 CC -1- SIMILARITY: Contains 1 PAN domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL, M74178; AAA50165.1; -  
 CC EMBL, U37055; AAC50471.1; -  
 CC EMBL, L11924; AAA59872.1; -  
 CC PIR, A40331; A47136.  
 CC HSSP, P00766; 1CHG.  
 CC MEROPS, S01.975; -  
 CC Genew, HNC:7380; MST1.  
 CC MIM, 142408; -  
 CC InterPro: IPR000001; Kringle.  
 CC InterPro: IPR003014; PAN.  
 CC InterPro: IPR003609; Pan app.  
 CC InterPro: IPR009003; Pept\_Ser\_Cys.  
 CC InterPro: IPR001254; Peptidase\_S1.  
 CC InterPro: IPR001314; Peptidase\_S1A.  
 CC Pfam, PF00051; Kringle; 4.  
 CC Pfam, PF00024; PAN; 1.  
 CC Pfam, PF00089; Trypsin; 1.  
 CC PRINTS, PR00722; CHYMOTRYPSIN.  
 CC PRINTS, PR00018; KRINGLE.  
 CC PRINTS, PR01505; PROTHROMBIN.  
 CC ProDom, PD000395; Kringle; 4.  
 CC SMART, SM00130; KR; 4.  
 CC SMART, SM00473; PAN\_AP; 1.  
 CC SMART, SM00020; TRYP\_SPC; 1.  
 CC PROSITE, PS00021; KRINGLE\_1; 4.  
 CC PROSITE, PS50070; KRINGLE\_2; 4.  
 CC PROSITE, PS50948; PAN; 1.  
 CC PROSITE, PS50240; TRYPSIN\_DOM; 1.  
 CC Direct protein sequencing; Glycoprotein; Kringle; Polymorphism;  
 CC Repeat; Serine protease homolog; Signal.  
 CC SIGNAL 1 18  
 CC CHAIN 19 711  
 CC DOMAIN 21 105  
 CC DOMAIN 110 186  
 CC DOMAIN 191 268  
 CC DOMAIN 283 361  
 CC DOMAIN 370 448  
 CC DOMAIN 484 711  
 CC DOMAIN 56 78  
 CC DISULFID 60 66  
 CC DISULFID 110 186  
 CC DISULFID 131 169  
 CC DISULFID 157 181  
 CC DISULFID 191 268  
 CC DISULFID 194 324  
 CC DISULFID 212 251  
 CC DISULFID 240 263  
 CC DISULFID 283 361  
 CC DISULFID 304 343  
 CC DISULFID 332 355  
 CC DISULFID 370 448  
 CC DISULFID 391 431  
 CC DISULFID 419 443  
 CC DISULFID 468 588

FT DISULFID 507 523 By similarity.  
 FT DISULFID 602 667 By similarity.  
 FT DISULFID 632 666 By similarity.  
 FT DISULFID 657 685 By similarity.  
 FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential)  
 FT CARBOHYD 296 296 N-linked (GlcNAc...) (Potential)  
 FT CARBOHYD 615 615 N-linked (GlcNAc...) (Potential)  
 FT VARIANT 13 13 Y -> C.  
 FT VARIANT 212 212 /FTID=VAR\_006631.  
 FT VARIANT 676 676 C -> F.  
 FT VARIANT 676 676 E -> K (in dbSNP:7798).  
 FT CONFLICT 292 292 /FTID=VAR\_014569.  
 FT CONFLICT 304 304 R -> G (in Ref. 3).  
 FT CONFLICT 306 306 C -> E (in Ref. 3).  
 FT CONFLICT 550 551 R -> E (in Ref. 3).  
 FT CONFLICT 593 593 PS -> ST (in Ref. 3).  
 FT CONFLICT 593 593 W -> E (in Ref. 3).  
 FT CONFLICT 623 623 L -> F (in Ref. 2).  
 SQ SEQUENCE 711 AA; 80379 MW; 596ED21F180290E4 CRC64;

Query Match 45.3%; Score 1180.5; DB 1; Length 711;  
 Best Local Similarity 47.4%; Pred. No. 3.7e-80;  
 Matches 197; Conservative 62; Mismatches 148; Indels 9; Gaps 4;

QY 33 VNTADQCANRCTRNGKLPFTCKAFVFDKARQCLTFPNSMSGVKEFGHEFDLYENKD 92  
 DB 50 VADAECAGRGRC---GPLMDGRAFHVNVSHGCCQLPWTQHSPTHRLRSRGCDLFOKXD 105  
 QY 93 YIRNCITCKGKSYKTVSITSGIKCPQSMWIMPHESFLLSSYRGLQENYCRNPGE 152  
 DB 106 YVRCITMNVGVGYRTAVTAVTGGLPCQAMSHKFPDHYKVTPLNNG--LEENFCNPGD 163  
 QY 153 EGGPWCFTSNPEVREVDIPQCSVEBCMTNGSGSYRGLMDHTSGKICQRMQDTPHRH 212  
 DB 164 PGGPWCYTTDAVRFQSGICSCREACVWNGEYRGAVRTSGRCQMDLQHPQH 223  
 DB 224 PFEPEKFLDQGLDDVYCNPDGSERPYCTTDPQLERFCDLPCGSAQROEA--TTV 281  
 QY 273 ECIQSGSGRYGTVTTNGIIPQRMDSQYRHEHDMTEFNKCDLRENYCRNPSSSP 332  
 DB 282 SCFRKGKGYRGTAATTAGVPCQRMDAQIHPHFTPEKACDLENFRCNPDGSAAP 341  
 QY 333 WCFTDPNIRGVYCSQIPNC-DMSHGDCYRGNGKNYGNISQTRSGLTCSMDKNMDDL 391  
 DB 342 WCFTLRPGRAFCQIRCTDDVRFQDCTHGAGEQYRGTYSKTRKGYOCQRMASRTHK 401  
 QY 392 HRHIFWEPDASKLNNYCRNPDDBAHGWCYTGNDLPMDYCPISRCGDTTPTIV 447  
 DB 402 PQFTTSPHQLLEENFCRNPDGSDHGPWCYTMDBRTFDFCALRCADDQPSIL 457

RESULT 15  
 ID P70006 PRELIMINARY; PRT; 717 AA.  
 AC P70006;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Hepatocyte growth factor-like protein precursor.  
 OS *Xenopus laevis* (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; *Xenopus*.  
 NCBI\_TaxID=8355;  
 RX MEDLINE=96404125; PubMed=8808403; DOI=10.1016/0925-4773(95)00458-0;  
 RA Aberger F., Schmidt G., Richter K.;  
 "The *Xenopus* homolog of hepatocyte growth factor-like protein is



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Best Local Similarity 99.8%; Pred. No. 5.5e-165;  
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNATADOCANRCTRNKGLPTCAFAFVFX 60  
:|||||  
Db 1 QKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNATADOCANRCTRNKGLPTCAFAFVFX 60

QY 61 ARKQCLMPFPMSSGSKVKEFGHEFDLYENKDYIRNCIIIGKRSYKGTIVSITKSGIKOP 120  
61 ARKQCLMPFPMSSGSKVKEFGHEFDLYENKDYIRNCIIIGKRSYKGTIVSITKSGIKOP 120

QY 121 WSSMTPIHSHSLPSSYRGKDLQENYCRNPRGEGGPMCTSNPEVRYEVCIDIPOCSEVFC 180  
121 WSSMTPIHSHSLPSSYRGKDLQENYCRNPRGEGGPMCTSNPEVRYEVCIDIPOCSEVFC 180

QY 181 MTCNGESYRGKDLMDHTESGKICQRMHDQTPHHRKFLPERYPDKGPDNYCRNPDGQPRWC 240  
181 MTCNGESYRGKDLMDHTESGKICQRMHDQTPHHRKFLPERYPDKGPDNYCRNPDGQPRWC 240

QY 241 YTLDPHTMEYCAIKTCADNTMNDTVDPLETTECIQGGEGYRGVTIWMGIPCORWDS 300  
241 YTLDPHTMEYCAIKTCADNTMNDTVDPLETTECIQGGEGYRGVTIWMGIPCORWDS 300

QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCTTDPNIRVGYCSQIPNCDSHGQDC 360  
301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCTTDPNIRVGYCSQIPNCDSHGQDC 360

QY 361 YRNGKNYMGNLQSTRSGLTCSMDKXMEDLHRHIFWEPDASKLNENYCRNPDGQPRWC 420  
361 YRNGKNYMGNLQSTRSGLTCSMDKXMEDLHRHIFWEPDASKLNENYCRNPDGQPRWC 420

QY 421 CYTGNPLIPMDYCPISRCGSDTTPITIV 447  
421 CYTGNPLIPMDYCPISRCGSDTTPITIV 447

Db 421 CYTGNPLIPMDYCPISRCGSDTTPITIV 447

RESULT 2  
ADM83266  
ID ADM83266 standard; protein; 447 AA.  
XX AC ADM83266;  
XX DT 18-NOV-2004 (first entry)  
XX DE Human NK4 protein #1.  
XX DE Human NK4 gene; neovascularisation; ovarian cancer; pancreatic cancer;  
KM stomach cancer; gallbladder cancer; renal cancer; prostatic cancer;  
KM breast cancer; esophageal cancer; hepatic cancer; oral cavity cancer;  
KM colon cancer; colorectal cancer; sarcoma; glioma; melanoma; gene therapy;  
KM human.  
XX OS Homo sapiens.  
XX PN US2003162736-A1.  
XX PD 28-AUG-2003.  
XX PF 27-SEP-2002; 2002US-00255649.  
XX PR 25-FEB-2002; 2002JP-00048644.  
XX PA (NAKA/) NAKAMURA T.  
XX PA (MATS/) MATSUMOTO K.  
XX PI Nakamura T, Matsumoto K;  
XX DR WPI, 2003-897946/82.  
XX DR N-PSDB; ADM83264.  
XX PT New NK4 gene, useful for producing a medicament for preventing or  
XX treating diseases caused by neovascularization, e.g. cancer.

PS Disclosure; Page 15-17; 27pp; English.  
XX CC The present invention provides a therapeutic agent NK4 polypeptides and  
XX their encoding polynucleotides. The invention is useful for producing a  
XX medicament for preventing or treating diseases caused by  
XX neovascularisation such as ovarian cancer, pancreatic cancer, stomach  
XX cancer, gallbladder cancer, renal cancer, prostatic cancer, breast  
XX cancer, esophageal cancer, hepatic cancer, oral cavity cancer, colon  
XX cancer, colorectal cancer, sarcoma, glioma and melanoma. The invention is  
XX also useful in gene therapy. The present sequence is human NK4 protein.  
SQ Sequence 447 AA;  
Query Match 99.9%; Score 2601; DB 7; Length 447;  
Best Local Similarity 99.8%; Pred. No. 5.5e-165;  
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNATADOCANRCTRNKGLPTCAFAFVFX 60  
:|||||  
Db 1 QKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNATADOCANRCTRNKGLPTCAFAFVFX 60

QY 61 ARKQCLMPFPMSSGSKVKEFGHEFDLYENKDYIRNCIIIGKRSYKGTIVSITKSGIKOP 120  
61 ARKQCLMPFPMSSGSKVKEFGHEFDLYENKDYIRNCIIIGKRSYKGTIVSITKSGIKOP 120

QY 121 WSSMTPIHSHSLPSSYRGKDLQENYCRNPRGEGGPMCTSNPEVRYEVCIDIPOCSEVFC 180  
121 WSSMTPIHSHSLPSSYRGKDLQENYCRNPRGEGGPMCTSNPEVRYEVCIDIPOCSEVFC 180

QY 181 MTCNGESYRGKDLMDHTESGKICQRMHDQTPHHRKFLPERYPDKGPDNYCRNPDGQPRWC 240  
181 MTCNGESYRGKDLMDHTESGKICQRMHDQTPHHRKFLPERYPDKGPDNYCRNPDGQPRWC 240

QY 241 YTLDPHTMEYCAIKTCADNTMNDTVDPLETTECIQGGEGYRGVTIWMGIPCORWDS 300  
241 YTLDPHTMEYCAIKTCADNTMNDTVDPLETTECIQGGEGYRGVTIWMGIPCORWDS 300

QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCTTDPNIRVGYCSQIPNCDSHGQDC 360  
301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCTTDPNIRVGYCSQIPNCDSHGQDC 360

QY 361 YRNGKNYMGNLQSTRSGLTCSMDKXMEDLHRHIFWEPDASKLNENYCRNPDGQPRWC 420  
361 YRNGKNYMGNLQSTRSGLTCSMDKXMEDLHRHIFWEPDASKLNENYCRNPDGQPRWC 420

QY 421 CYTGNPLIPMDYCPISRCGSDTTPITIV 447  
421 CYTGNPLIPMDYCPISRCGSDTTPITIV 447

Db 421 CYTGNPLIPMDYCPISRCGSDTTPITIV 447

RESULT 3  
AA98485  
ID AA98485 standard; protein; 697 AA.  
XX AC AA98485;  
XX DT 31-JUL-2000 (first entry)  
XX DE Hepatocyte growth factor HGF used in nucleic acid transporter system.  
XX KM Transporter system; nucleic acid delivery; gene therapy; cancer;  
XX KM carcinogenesis; cardiovascular disease; infection.  
XX OS Synthetic.  
XX PN US6033884-A.  
XX PD 07-MAR-2000.  
XX PF 14-DEC-1993; 93US-00167641.  
XX PR 20-MAR-1992; 92US-00855389.  
XX PR 19-MAR-1993; 93WO-US002725.



Db 181 MTCNGESYRGIMDHTESGKICQRMWDHQTPHRHKFLPERYPDKGFDNYCRNPDGQPRPWC 240  
Qy 241 YTLDPHTRWEXCAIKTCADNTMNDTVPLETTTECIQGGEGYRGVNTIWMGIFCQWRDS 300  
Db 241 YTLDPHTRWEXCAIKTCADNTMNDTVPLETTTECIQGGEGYRGVNTIWMGIFCQWRDS 300  
Qy 301 QYPHEHMTPEPFCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
Db 301 QYPHEHMTPEPFCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
Qy 361 YRGNKKNYMGSLQSTRSGLTCSMDKNMEDLHRHIFWEPDASKLKNENYCRNPDHAGPW 420  
Db 361 YRGNKKNYMGSLQSTRSGLTCSMDKNMEDLHRHIFWEPDASKLKNENYCRNPDHAGPW 420  
Qy 421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447  
Db 421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447

## RESULT 5

AAB45838  
ID AAB45838 standard; protein; 697 AA.

AA45838;  
AC

21-MAR-2001 (first entry)

Nucleic acid transporter system peptide ligand SEQ ID NO 50.

Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme;  
growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene;  
tumor antigen; tumor suppressor; viral antigen; parasitic antigen;  
bacterial antigen.

Unidentified.

US6150168-A.

21-NOV-2000.

05-JUN-1995; 95US-00460971.

20-MAR-1992; 92US-00855389.

19-MAR-1993; 93WO-US002725.

14-DEC-1993; 93US-00167641.

(BAYU ) BAYLOR COLLEGE MEDICINE.

Gottchalk S, Sparrow J, Cristiano RJ, Smith LC, Woo SLC;  
WPI, 2001-049093/06.

Nucleic acid transporter system for delivering nucleic acid into a cell,  
useful for delivering proteins and polypeptides to cells, including  
growth factors, enzymes, hormones, and tumor suppressors.

Claim 8; Col 115-118; 105pp; English.

This invention describes a novel system (I) for delivering a nucleic acid  
to a cell, comprising a binding complex comprising a ligand binding  
molecule noncovalently bound to a nucleic acid and covalently linked to a  
surface ligand, and a second binding complex comprising a second binding  
molecule noncovalently bound to a nucleic acid and covalently linked to a  
nuclear ligand. The complexes are simultaneously bound to the nucleic  
acid. The nucleic acid transporter system can also be used in a method  
for the in vivo targeting of the insertion of DNA into a cell. It can  
also be used in processes for producing transformed cell lines. The  
system can be used to deliver a variety of proteins and polypeptides,  
such as hormones, growth factors, enzymes, clotting factors,  
apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor  
suppressors, viral antigens, parasitic antigens, and bacterial antigens.  
The transporter system uses lysis agents to overcome the problems of  
endosomal/lysosomal degradation seen with prior art systems

XX  
SQ Sequence 697 AA;

Query Match 99.9%; Score 2601; DB 4; Length 697;  
Best Local Similarity 99.8%; Pred. No. 8.7e-165;  
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERKRNTIHEFKSAKTLIKIDPALKIKTKKVTADOCANRCTRNKGLPFTCAVFDK 60  
Db 1 QRRKNTIHEFKSAKTLIKIDPALKIKTKKVTADOCANRCTRNKGLPFTCAVFDK 60  
Qy 61 ARKOCCLMPFNSSSGYKKEFGHEFDLYENKDYIRNCIIGKNSYKGTVSITKSGICOP 120  
Db 61 ARKOCCLMPFNSSSGYKKEFGHEFDLYENKDYIRNCIIGKNSYKGTVSITKSGICOP 120  
Qy 121 WSSMIPEHSHFLPSYRGKDLQENYCRNPRGEGSPWCFTSNPEVRVECDIPQCEVEVC 180  
Db 121 WSSMIPEHSHFLPSYRGKDLQENYCRNPRGEGSPWCFTSNPEVRVECDIPQCEVEVC 180  
Qy 181 MTCNGESYRGIMDHTESGKICQRMWDHQTPHRHKFLPERYPDKGFDNYCRNPDGQPRPWC 240  
Db 181 MTCNGESYRGIMDHTESGKICQRMWDHQTPHRHKFLPERYPDKGFDNYCRNPDGQPRPWC 240  
Qy 241 YTLDPHTRWEXCAIKTCADNTMNDTVPLETTTECIQGGEGYRGVNTIWMGIFCQWRDS 300  
Db 241 YTLDPHTRWEXCAIKTCADNTMNDTVPLETTTECIQGGEGYRGVNTIWMGIFCQWRDS 300  
Qy 301 QYPHEHMTPEPFCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
Db 301 QYPHEHMTPEPFCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
Qy 361 YRGNKKNYMGSLQSTRSGLTCSMDKNMEDLHRHIFWEPDASKLKNENYCRNPDHAGPW 420  
Db 361 YRGNKKNYMGSLQSTRSGLTCSMDKNMEDLHRHIFWEPDASKLKNENYCRNPDHAGPW 420  
Qy 421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447  
Db 421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447

## RESULT 6

AAU04275  
ID AAU04275 standard; peptide; 697 AA.

AAU04275;  
AC

23-OCT-2001 (first entry)

Nuclear ligand Peg20 used in nucleic acid transporter system.

Nucleic acid transport; cytosols; ligand; lysis agent; spacer molecule;  
gene therapy; hepatocyte; muscle; bone forming cell.

Synthetic.

US6177554-B1.

23-JAN-2001.

05-JUN-1995; 95US-00462040.

20-MAR-1992; 92US-00855389.

19-MAR-1993; 93WO-US002725.

14-DEC-1993; 93US-00167641.

(BAYU ) BAYLOR COLLEGE MEDICINE.

Woo SLC, Smith LC, Cristiano RJ, Gottchalk S, Sparrow J;  
WPI, 2001-365933/38.

Nucleic acid transporter system, useful for creating transgenic animals for  
assessing human disease such as cancer in an animal model.



XX XX Disclosure; Fig 23A; 11pp; English.  
PS XX  
CC The sequence represents the nuclear ligand, Pep20, used in a nucleic acid  
CC transporter system. The nucleic acid transporter system uses nucleic acid  
CC binding complexes containing surface ligands which are capable of binding  
CC to a cell surface receptor and entering the cell through cytolysis. The  
CC compounds of the invention are either ligands, binding molecules (surface  
CC ligands), lysis agents, spacer molecules or their intermediates. The  
CC ligands, binding molecules, lysis agents and spacer molecules are used in  
CC nucleic acid transporter systems to deliver nucleic acid into specific  
CC cells e.g. in gene therapy to deliver nucleic acid into hepatocytes,  
CC muscle cells or bone forming cells  
XX  
SQ Sequence 697 AA;  
Query Match 99.9%; Score 2601; DB 4; Length 697;  
Best Local Similarity 99.8%; Pred. No. 8.7e-165;  
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ERKRRNTIHEFKSAKTLTIKIDPALKIKTKKVNNTADQCANRCTRNGKLPFTCKAFVPDK 60  
DB 1 QKRRNTIHEFKSAKTLTIKIDPALKIKTKKVNNTADQCANRCTRNGKLPFTCKAFVPDK 60  
QY 61 ARKQCIWPPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITKSGIKCOP 120  
DB 61 ARKQCIWPPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITKSGIKCOP 120  
QY 121 WSSMI PHEHSFLPSSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDI PQCESEVFC 180  
DB 121 WSSMI PHEHSFLPSSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDI PQCESEVFC 180  
QY 181 MTCNGESYRGKDLMDHTESGKICQRMWHQTPHRHKLPERYPDKGFDNRYCRNPDGQRPWC 240  
DB 181 MTCNGESYRGKDLMDHTESGKICQRMWHQTPHRHKLPERYPDKGFDNRYCRNPDGQRPWC 240  
QY 241 YLDPHTRWYCAIKTCADNTMNDTVPLETTETCIQOGGEGYRGVTNTIWNIGIPCORWDS 300  
DB 241 YLDPHTRWYCAIKTCADNTMNDTVPLETTETCIQOGGEGYRGVTNTIWNIGIPCORWDS 300  
QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
DB 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
QY 361 YGNGKNYVGNLSQTRSGLTCSMDKKNMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 420  
DB 361 YGNGKNYVGNLSQTRSGLTCSMDKKNMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 420  
QY 421 CYTGNPLIPWDYCPISRCEGDTPTTIV 447  
DB 421 CYTGNPLIPWDYCPISRCEGDTPTTIV 447  
RESULT 7  
ID AAR25676  
AA AAR25676 standard; protein; 728 AA.  
AC AAR25676;  
XX  
XX 20-JAN-1993 (first entry)  
XX  
DE Recombinant human hepatocyte growth factor.  
XX  
DE HGF; enhance growth; preparing transgenic animals; hepatic disease;  
XX clinical diagnostic reagent; drug.  
XX  
XX Homo sapiens.  
XX OS  
XX JP04183394-A.  
XX PN  
XX 30-JUN-1992.  
XX PD  
XX 19-NOV-1990; 90JP-00314548.  
XX PF

XX XX 19-NOV-1990; 90JP-00314548.  
XX PR  
XX (TOYO) TOYOBO KK.  
XX PA (NAKA/) NAKAMURA T.  
XX DR WPI; 1992-265591/32.  
XX  
XX Recombinant human hepatocyte growth factor and DNA encoding it - useful  
XX PT for diagnosis and treatment of hepatic disease and transgenic animal  
XX PT prepn.  
XX  
XX Disclosure; Page 11; 28pp; Japanese.  
PS  
XX  
XX  
CC This sequence represents a recombinant human hepatocyte growth factor. It  
CC has physiological activity, and using it enhanced growth of hepatocytes  
CC is possible. It is useful as a clinical diagnostic reagent, or a drug for  
CC treating hepatic disease. See also AAR25676-92, AAO26713-27  
XX  
SQ Sequence 728 AA;  
Query Match 99.9%; Score 2601; DB 2; Length 728;  
Best Local Similarity 99.8%; Pred. No. 9.1e-165;  
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ERKRRNTIHEFKSAKTLTIKIDPALKIKTKKVNNTADQCANRCTRNGKLPFTCKAFVPDK 60  
DB 32 QKRRNTIHEFKSAKTLTIKIDPALKIKTKKVNNTADQCANRCTRNGKLPFTCKAFVPDK 91  
QY 61 ARKQCIWPPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITKSGIKCOP 120  
DB 61 ARKQCIWPPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITKSGIKCOP 151  
QY 92 ARKQCIWPPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITKSGIKCOP 151  
DB 92 ARKQCIWPPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITKSGIKCOP 151  
QY 121 WSSMI PHEHSFLPSSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDI PQCESEVFC 180  
DB 121 WSSMI PHEHSFLPSSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDI PQCESEVFC 211  
QY 152 WSSMI PHEHSFLPSSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDI PQCESEVFC 211  
DB 152 WSSMI PHEHSFLPSSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCDI PQCESEVFC 211  
QY 181 MTCNGESYRGKDLMDHTESGKICQRMWHQTPHRHKLPERYPDKGFDNRYCRNPDGQRPWC 240  
DB 181 MTCNGESYRGKDLMDHTESGKICQRMWHQTPHRHKLPERYPDKGFDNRYCRNPDGQRPWC 271  
QY 212 MTCNGESYRGKDLMDHTESGKICQRMWHQTPHRHKLPERYPDKGFDNRYCRNPDGQRPWC 271  
DB 212 MTCNGESYRGKDLMDHTESGKICQRMWHQTPHRHKLPERYPDKGFDNRYCRNPDGQRPWC 271  
QY 241 YLDPHTRWYCAIKTCADNTMNDTVPLETTETCIQOGGEGYRGVTNTIWNIGIPCORWDS 300  
DB 241 YLDPHTRWYCAIKTCADNTMNDTVPLETTETCIQOGGEGYRGVTNTIWNIGIPCORWDS 331  
QY 272 YLDPHTRWYCAIKTCADNTMNDTVPLETTETCIQOGGEGYRGVTNTIWNIGIPCORWDS 331  
DB 272 YLDPHTRWYCAIKTCADNTMNDTVPLETTETCIQOGGEGYRGVTNTIWNIGIPCORWDS 331  
QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
DB 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 391  
QY 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 391  
DB 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 391  
QY 361 YGNGKNYVGNLSQTRSGLTCSMDKKNMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 420  
DB 361 YGNGKNYVGNLSQTRSGLTCSMDKKNMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 451  
QY 421 CYTGNPLIPWDYCPISRCEGDTPTTIV 447  
DB 421 CYTGNPLIPWDYCPISRCEGDTPTTIV 478  
RESULT 8  
ID AAR20005  
AA AAR20005 standard; protein; 728 AA.  
AC AAR20005;  
XX  
XX 24-MAR-1992 (first entry)  
XX  
DE Human hepatocyte growth factor.  
XX  
DE HGF; kidney regeneration; nephritis.  
XX  
XX Homo sapiens.  
XX OS  
XX EP462549-A.  
XX PN

```
XX 27-DEC-1991.
PD 18-JUN-1991; 91EP-00109923.
XX 18-JUN-1991; 91EP-00109923.
XX 19-JUN-1990; 90JP-00158841.
XX (TOYM ) TOYO BOSEKI KK.
XX Nakamuro T;
XX WPI; 1992-000939/01.
DR N-PSDB; AAQ020049.
XX Agent contg. hepatocyte growth factor and carrier - used for treating
PT renal diseases and promoting nephrocyte growth and as diagnostic for
PT renal diseases.
XX Disclosure; Fig 1; 15pp; English.
XX PS
XX CC Human HGF comprises an alpha-chain of 440 amino acids and a beta-chain of
CC 234 amino acids. There are 4 kringe domains in the alpha-chain, similar
CC to that of plasmin; the beta-chain has about 37 per cent homology with
CC the beta-chain of plasmin having serine protease activity. Homology of
CC the amino acid sequence of rat HGF and human HGF is 91.6 per cent in the
CC alpha-chain and 88.9 per cent in the beta-chain. HGF has been found to be
CC an agent for nephrocyte growth and is useful as a treatment for renal
CC failure
XX
XX SQ Sequence 728 AA;
Query Match 99.9%; Score 2601; DB 2; Length 728;
Best Local Similarity 99.8%; Pred. No. 9.1e-165;
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ERKRRNTTHERFKSAKTLIKIDPALKITKKVNTADOCANRCTRNKGLPTCKAFVFDK 60
DB :
DB 32 QKRKRNTTHERFKSAKTLIKIDPALKITKKVNTADOCANRCTRNKGLPTCKAFVFDK 91
QY 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKOP 120
DB 92 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKOP 151
QY 121 WSSMTIPHESFLPSSSYRGKDLQENYCRNPRGEGGPMCTSNPEVRYEVCDIPOCSEYEC 180
DB 152 WSSMTIPHESFLPSSSYRGKDLQENYCRNPRGEGGPMCTSNPEVRYEVCDIPOCSEYEC 211
QY 181 MTCNGESYRGKDLMDHTESGKICQRMWHQTPHRHKLPERYPDKGFDNDCRNPDGQPRPMC 240
DB 212 MTCNGESYRGKDLMDHTESGKICQRMWHQTPHRHKLPERYPDKGFDNDCRNPDGQPRPMC 271
QY 241 YTLDPHTRWYCAITCADNTMNDVPLETTECIQGGGEGYRGVNTIWNIGIPQCRWDS 300
DB 272 YTLDPHTRWYCAITCADNTMNDVPLETTECIQGGGEGYRGVNTIWNIGIPQCRWDS 331
QY 301 QYPHEHDMTPENFKCDLRENYCRNPDGSESPWCTTDPNIRVGYCSQIPNCDMSHGQDC 360
DB 332 QYPHEHDMTPENFKCDLRENYCRNPDGSESPWCTTDPNIRVGYCSQIPNCDMSHGQDC 391
QY 361 YRNGNGNTWGNLSQTRSGITCSMWDMKMDLHRHIFWEPDASKLLENYCRNPDGDAHGW 420
DB 392 YRNGNGNTWGNLSQTRSGITCSMWDMKMDLHRHIFWEPDASKLLENYCRNPDGDAHGW 451
QY 421 CYTGNPLIPWDYCPISRCGEGDTPPTIV 447
DB 452 CYTGNPLIPWDYCPISRCGEGDTPPTIV 478
RESULT 9
ID AAR40862 standard; protein; 728 AA.
XX
AC AAR40862;
```

```
XX 14-MAR-1994 (first entry)
DT Competitive inhibitor of HGF.
XX
DE HGF, hepatocyte growth factor; transformation; antagonistic; liver disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..31
XX Protein /label= sig_peptide
XX /label= 32..728
XX /label= mat_protein
XX Misc-difference 494
XX /note= "site of possible mutation"
XX
XX JP05208998-A.
XX
XX 20-AUG-1993.
XX
XX 25-DEC-1991; 91JP-00357040.
XX
XX 25-DEC-1991; 91JP-00357040.
XX
XX (MITU ) MITSUBISHI KASEI CORP.
XX
XX WPI; 1993-297806/38.
XX N-PSDB; AAQ47832.
XX
XX New protein is competitive inhibitor of hepatocyte growth factor - used
XX in animal model of liver disease.
XX
XX Claim 7; Page 8-11; 20pp; Japanese.
XX
XX The gene encodes an inhibitor of HGF, which has a molecular weight of ca.
XX 76000 to 92000 as determined by SDS-PAGE. Human modified (NP) HGF-A and
XX B fragments were prepared from human HGF cDNA. This was amplified by PCR
XX to give a human NP-HGF DNA fragment that was transformed into E.coli.
XX (see AAQ47833) for a related sequence
XX
XX SQ Sequence 728 AA;
Query Match 99.9%; Score 2601; DB 2; Length 728;
Best Local Similarity 99.8%; Pred. No. 9.1e-165;
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ERKRRNTTHERFKSAKTLIKIDPALKITKKVNTADOCANRCTRNKGLPTCKAFVFDK 60
DB :
DB 32 QKRKRNTTHERFKSAKTLIKIDPALKITKKVNTADOCANRCTRNKGLPTCKAFVFDK 91
QY 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKOP 120
DB 92 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKOP 151
QY 121 WSSMTIPHESFLPSSSYRGKDLQENYCRNPRGEGGPMCTSNPEVRYEVCDIPOCSEYEC 180
DB 152 WSSMTIPHESFLPSSSYRGKDLQENYCRNPRGEGGPMCTSNPEVRYEVCDIPOCSEYEC 211
QY 181 MTCNGESYRGKDLMDHTESGKICQRMWHQTPHRHKLPERYPDKGFDNDCRNPDGQPRPMC 240
DB 212 MTCNGESYRGKDLMDHTESGKICQRMWHQTPHRHKLPERYPDKGFDNDCRNPDGQPRPMC 271
QY 241 YTLDPHTRWYCAITCADNTMNDVPLETTECIQGGGEGYRGVNTIWNIGIPQCRWDS 300
DB 272 YTLDPHTRWYCAITCADNTMNDVPLETTECIQGGGEGYRGVNTIWNIGIPQCRWDS 331
QY 301 QYPHEHDMTPENFKCDLRENYCRNPDGSESPWCTTDPNIRVGYCSQIPNCDMSHGQDC 360
DB 332 QYPHEHDMTPENFKCDLRENYCRNPDGSESPWCTTDPNIRVGYCSQIPNCDMSHGQDC 391
QY 361 YRNGNGNTWGNLSQTRSGITCSMWDMKMDLHRHIFWEPDASKLLENYCRNPDGDAHGW 420
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Db 392 YRNGKNYVGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDAHGPM 451
QY 421 CYTGNPLIPWDYCPISRCBGDTTPTIV 447
Db 452 CYTGNPLIPWDYCPISRCBGDTTPTIV 478

RESULT 10
AAR40863
ID AAR40863 standard; protein; 728 AA.
XX AAR40863;
AC AAR40863;
XX 14-MAR-1994 (first entry)
XX 14-MAR-1994 (first entry)
DE Competitive inhibitor of HGF.
XX HGF, hepatocyte growth factor; transformation; antagonist; liver disease.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..31
FT /label= sig_peptide
FT Protein 32..728
FT /label= mat_protein
FT Misc-difference 489
FT /note= "site of possible mutation"
FT Misc-difference 491
FT /note= "site of possible mutation"
FT Misc-difference 494
FT /note= "site of possible mutation"
XX JP05208998-A.
XX 20-AUG-1993.
XX 25-DEC-1991; 91JP-00357040.
XX 25-DEC-1991; 91JP-00357040.
XX 25-DEC-1991; 91JP-00357040.
XX (MITU ) MITSUBISHI KASEI CORP.
XX WPI; 1993-297806/38.
XX DR N-PSDB; AAQ47833.
XX PT New protein is competitive inhibitor of hepatocyte growth factor - used
XX in animal model of liver disease.
XX PS Claim 6; Page 11-14; 20pp; Japanese.
XX CC The gene encodes an inhibitor of HGF, which has a molecular weight of ca.
XX 76000 to 92000 as determined by SDS-PAGE. Human modified (NP) HGF-A and -
XX B fragments were prepared from human HGF CDNA. This was amplified by PCR
XX to give a human NP-HGF DNA fragment that was transformed into E.coli.
XX (see AAQ47833) for a related sequence
XX SQ Sequence 728 AA;

Query Match 99.9%; Score 2601; DB 2; Length 728;
Best Local Similarity 99.8%; Pred. No. 9.1e-165;
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKKRRNTHEPKRSATTLIKIDPAKITKKVNTADOCANRCTRKKGLPTCKAFVFK 60
Db 32 QKRRNTHEPKRSATTLIKIDPAKITKKVNTADOCANRCTRKKGLPTCKAFVFK 91
QY 61 ARKQCLMPFPNMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGVTSITKSGIKOP 120
Db 92 ARKQCLMPFPNMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGVTSITKSGIKOP 151
QY 121 WSGMIFHEHSFLPSSYRGKDLQENYCRNPGEGBGFWCFTSNPEVRYEVCIDIPOCSEVEC 180
```

```
Db 152 WSGMIFHEHSFLPSSYRGKDLQENYCRNPGEGBGFWCFTSNPEVRYEVCIDIPOCSEVEC 211
QY 181 MTONGESYRGKDLMDHTESGKICORMDHQTPHRKFLPERYPDGFDNNYCRNPDGQRPWC 240
Db 212 MTONGESYRGKDLMDHTESGKICORMDHQTPHRKFLPERYPDGFDNNYCRNPDGQRPWC 271
QY 241 YTLDPHTMEYCAIKTCADNTMNDTVPLETTTCIQGQEGYRGVTNIWNGIPCORWMS 300
Db 272 YTLDPHTMEYCAIKTCADNTMNDTVPLETTTCIQGQEGYRGVTNIWNGIPCORWMS 331
QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESWCFTTDPNIRVYCSQIPNCDMSGQDC 360
Db 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESWCFTTDPNIRVYCSQIPNCDMSGQDC 391
QY 361 YRNGKNYVGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDAHGPM 420
Db 392 YRNGKNYVGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDAHGPM 451
QY 421 CYTGNPLIPWDYCPISRCBGDTTPTIV 447
Db 452 CYTGNPLIPWDYCPISRCBGDTTPTIV 478

RESULT 11
AAR42062
ID AAR42062 standard; protein; 728 AA.
XX AAR42062;
AC AAR42062;
XX 25-MAR-2003 (revised)
XX 15-NOV-1993 (first entry)
XX Vascular endothelial cell growth enhancer protein.
XX DE Enhance; growth; vascular endothelial cell; human; tumour; cell line;
XX HUOCA-II; HUOCA-III; blood vessel; wounds; burns; decubitus;
XX post-operative tissue damage; drug; cardiac angiopathy.
XX OS Homo sapiens.
XX EP550296-A2.
XX 07-JUL-1993.
XX 27-NOV-1992; 92EP-00403199.
XX 28-NOV-1991; 91JP-00337999.
XX (TERU ) TERUMO CORP.
XX PI Sudo T, Harada K, Hirahara I, Adachi M;
XX WPI; 1993-215669/27.
XX DR N-PSDB; AAQ45702.
XX PT Vascular endothelial cell growth factor protein - used for promoting
XX angiogenesis in the treatment of cardiac angiopathy, wounds, burn
XX injuries, postoperative tissue damage etc.
XX PS Claim 6; Page 18-21; 44pp; English.
XX CC This sequence represents a single chain protein which selectively
XX enhances the growth of vascular endothelial cells. This protein was
XX produced by the human tumour cell line HUOCA-II or HUOCA-III. This
XX protein enhances the formation of new blood vessels and may be used to
XX enhance healing of wounds, burns injuries, decubitus or post-operative
XX tissue damage. It may also be used as a drug for cardiac angiopathy.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 728 AA;

Query Match 99.9%; Score 2601; DB 2; Length 728;
Best Local Similarity 99.8%; Pred. No. 9.1e-165;
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Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRNTIHERKSAKTTLIKIDPALKIKTKKVTADQCANCTRNKGLPFTCAFAVFDK 60  
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QY 61 ARKQCLMPFPMSMSGVKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKQCP 120  
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Db 92 ARKQCLMPFPMSMSGVKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKQCP 151

QY 121 WSSMI.PHEHSFL.PSSYRGKDLQENYCRNPRGEGGPGWCFSTNPEVRYEVCDI.PQCSVEVC 180  
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Db 152 WSSMI.PHEHSFL.PSSYRGKDLQENYCRNPRGEGGPGWCFSTNPEVRYEVCDI.PQCSVEVC 211

QY 181 MTCNGESYRGMLMDHTESGKICQRMWDQTPRHAKFLPERYPDKGPDNYCRNPDGQPRPWC 240  
:|||||  
Db 212 MTCNGESYRGMLMDHTESGKICQRMWDQTPRHAKFLPERYPDKGPDNYCRNPDGQPRPWC 271

QY 241 YTLDPHTRWEXCAITKCADNTMNDVPLETTECIQGGEGYRGTVNTIWMGIPQQRWDS 300  
:|||||  
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QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
:|||||  
Db 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 391

QY 361 YRGNGKNYMGNL.SQTRSGLTCSMDKXMDLHRHIFWEPDASKLNNYCRNPDHDAHGPW 420  
:|||||  
Db 392 YRGNGKNYMGNL.SQTRSGLTCSMDKXMDLHRHIFWEPDASKLNNYCRNPDHDAHGPW 451

QY 421 CYTGNPLIPWDYCPISRCEGDTPTIV 447  
:|||||  
Db 452 CYTGNPLIPWDYCPISRCEGDTPTIV 478

RESULT 12  
AAR87522  
ID AAR87522 standard; protein: 728 AA.

AC AAR87522;  
XX  
DT 21-JUN-1996 (first entry)

DE Mutant hepatocyte growth factor #1 with changes at residues 491-495.  
XX  
KW Hepatocyte growth factor; protease; cleavage recognition site; Factor Xa;  
XX injury; blood vessel; point mutation.  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT Misc-difference 491..495  
FT /note="change from wild type sequence: Lys-Glu-Leu-Arg-  
FT Val to Ile-Glu-Gly-Arg-Thr"  
XX  
XX JP07304796-A.  
XX  
XX 21-NOV-1995.  
XX  
XX 07-MAY-1994; 94JP-00117506.  
XX  
XX 07-MAY-1994; 94JP-00117506.  
XX  
XX (TERU ) TERUMO CORP.  
XX  
XX PA  
XX WPI; 1996-035890/04.  
XX  
XX DR  
XX  
XX Novel derivative of hepatocyte growth factor - comprises a mutation at  
XX PT positions 492-494, for use in treating injured blood vessels.  
XX  
XX PS  
XX Disclosure; Page; 8pp; Japanese.  
XX  
XX CC The amino acid of the hepatocyte growth factor (HGF) generated to contain

CC amino acid changes at residues 492-494. (Note - this sequence is not  
CC given in the specification but is based on the HGF sequence given in  
CC AAR0005). The generated mutant contains the sequence Ile-Glu-Gly-Arg-  
CC Thr, which replaces the wild type sequence Lys-Glu-Leu-Arg-Val. The HGF  
CC is translated as single chain protein which is activated to a two chain  
CC protein by protease cleavage between residues 494-5, producing the alpha  
CC and beta chains. The novel sequence alters the protease recognition site,  
CC putatively introducing a Factor Xa recognition site. The novel HGF deriv.  
CC can be activated specifically at the site of injury in a blood vessel.  
CC (See AAR87522-5 for different HGF derivs.). The novel HGF derivs. were  
CC generated by point mutations using the oligonucleotides AAT06762-5  
XX  
SQ Sequence 728 AA;

Query Match 99.9%; Score 2601; DB 2; Length 728;  
Best Local Similarity 99.8%; Pred. No. 9.1e-165;  
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRNTIHERKSAKTTLIKIDPALKIKTKKVTADQCANCTRNKGLPFTCAFAVFDK 60  
:|||||  
Db 32 QKRKRNTIHERKSAKTTLIKIDPALKIKTKKVTADQCANCTRNKGLPFTCAFAVFDK 91

QY 61 ARKQCLMPFPMSMSGVKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKQCP 120  
:|||||  
Db 92 ARKQCLMPFPMSMSGVKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKQCP 151

QY 121 WSSMI.PHEHSFL.PSSYRGKDLQENYCRNPRGEGGPGWCFSTNPEVRYEVCDI.PQCSVEVC 180  
:|||||  
Db 152 WSSMI.PHEHSFL.PSSYRGKDLQENYCRNPRGEGGPGWCFSTNPEVRYEVCDI.PQCSVEVC 211

QY 181 MTCNGESYRGMLMDHTESGKICQRMWDQTPRHAKFLPERYPDKGPDNYCRNPDGQPRPWC 240  
:|||||  
Db 212 MTCNGESYRGMLMDHTESGKICQRMWDQTPRHAKFLPERYPDKGPDNYCRNPDGQPRPWC 271

QY 241 YTLDPHTRWEXCAITKCADNTMNDVPLETTECIQGGEGYRGTVNTIWMGIPQQRWDS 300  
:|||||  
Db 272 YTLDPHTRWEXCAITKCADNTMNDVPLETTECIQGGEGYRGTVNTIWMGIPQQRWDS 331

QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
:|||||  
Db 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 391

QY 361 YRGNGKNYMGNL.SQTRSGLTCSMDKXMDLHRHIFWEPDASKLNNYCRNPDHDAHGPW 420  
:|||||  
Db 392 YRGNGKNYMGNL.SQTRSGLTCSMDKXMDLHRHIFWEPDASKLNNYCRNPDHDAHGPW 451

QY 421 CYTGNPLIPWDYCPISRCEGDTPTIV 447  
:|||||  
Db 452 CYTGNPLIPWDYCPISRCEGDTPTIV 478

RESULT 13  
AAR87524  
ID AAR87524 standard; protein: 728 AA.

AC AAR87524;  
XX  
DT 21-JUN-1996 (first entry)

DE Mutant hepatocyte growth factor #3 with changes at residues 491-495.  
XX  
KW Hepatocyte growth factor; protease; cleavage recognition site; Factor Xa;  
XX injury; blood vessel; point mutation.  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT Misc-difference 491..495  
FT /note="change from wild type sequence: Lys-Glu-Leu-Arg-  
FT Val to Lys-Glu-Gly-Arg-Thr"  
XX  
XX JP07304796-A.  
XX

PD 21-NOV-1995.  
 XX  
 XX 07-MAY-1994; 94JP-00117506.  
 XX  
 PR 07-MAY-1994; 94JP-00117506.  
 XX  
 PA (TERU ) TERUMO CORP.  
 XX  
 DR WPI; 1996-035890/04.  
 XX  
 PT Novel derivative of hepatocyte growth factor - comprises a mutation at  
 positions 492-494, for use in treating injured blood vessels.  
 XX  
 PS Disclosure; Page; 8pp; Japanese.  
 XX  
 CC The amino acid of the hepatocyte growth factor (HGF) generated to contain  
 CC amino acid changes at residues 492-494. (Note - this sequence is not  
 CC given in the specification but is based on the HGF sequence given in  
 CC AAR20005). The generated mutant contains the sequence Lys-Gln-Gly-Arg-  
 CC Thr, which replaces the wild type sequence Lys-Glu-Leu-Arg-Val. The HGF  
 CC is translated as single chain protein which is activated to a two chain  
 CC protein by protease cleavage between residues 494-5, producing the alpha  
 CC and beta chains. The novel sequence alters the protease recognition site,  
 CC putatively introducing a Factor Xa recognition site. The novel HGF deriv.  
 CC can be activated specifically at the site of injury in a blood vessel.  
 CC (See AAR87522-5 for different HGF derivs.). The novel HGF derivs. were  
 CC generated by point mutations using the oligonucleotides AAT06762-5  
 XX  
 SQ Sequence 728 AA;

Query Match 99.9%; Score 2601; DB 2; Length 728;  
 Best Local Similarity 99.8%; Pred. No. 9.1e-165;  
 Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERRRRNTIIEFKSAKTTLIKIDPAKIKTKKVNNTADQCANRCTRNKGLPFTCKAVFPDK 60  
 DB 32 QRRRRNTIIEFKSAKTTLIKIDPAKIKTKKVNNTADQCANRCTRNKGLPFTCKAVFPDK 91  
 QY 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKCOP 120  
 DB 92 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKCOP 151  
 QY 121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCEVEVC 180  
 DB 152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCEVEVC 211  
 QY 181 MTCNGSYRGKDLMDHTESGKICORWDHQTPIRHKFLPERYPDKGFDNRYCRNPDGQRPWC 240  
 DB 212 MTCNGSYRGKDLMDHTESGKICORWDHQTPIRHKFLPERYPDKGFDNRYCRNPDGQRPWC 271  
 QY 241 YTLDPHTRWECYAIKTCADNTMNDTVPLETTETCIQOGGEGYRGVTNTIWNIGIPCGRWMS 300  
 DB 272 YTLDPHTRWECYAIKTCADNTMNDTVPLETTETCIQOGGEGYRGVTNTIWNIGIPCGRWMS 331  
 QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGDQC 360  
 DB 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGDQC 391  
 QY 361 YRNGNGKNTMGNLSQTSGLTCSWMDXQMEDLHRHIWEPPDASKLANENYCRNPDDAHGPW 420  
 DB 392 YRNGNGKNTMGNLSQTSGLTCSWMDXQMEDLHRHIWEPPDASKLANENYCRNPDDAHGPW 451  
 QY 421 CYTGNPLIPWDYCPISRCGDDTPTIV 447  
 DB 452 CYTGNPLIPWDYCPISRCGDDTPTIV 478

RESULT 14  
 AAR87525  
 ID AAR87525 standard; protein; 728 AA.  
 XX  
 AC AAR87525;  
 XX

DT 21-JUN-1996 (first entry)  
 XX  
 XX Mutant hepatocyte growth factor #4 with changes at residues 491-495.  
 DE  
 XX Hepatocyte growth factor; protease; cleavage recognition site; Factor Xa;  
 KM injury; blood vessel; point mutation.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 491..495  
 FT Val to Lys-Gln-Gly-Arg-Val  
 XX  
 XX JP07304796-A.  
 XX  
 PD 21-NOV-1995.  
 XX  
 PF 07-MAY-1994; 94JP-00117506.  
 XX  
 PR 07-MAY-1994; 94JP-00117506.  
 XX  
 PA (TERU ) TERUMO CORP.  
 XX  
 DR WPI; 1996-035890/04.  
 XX  
 PT Novel derivative of hepatocyte growth factor - comprises a mutation at  
 positions 492-494, for use in treating injured blood vessels.  
 XX  
 PS Disclosure; Page; 8pp; Japanese.  
 XX  
 CC The amino acid of the hepatocyte growth factor (HGF) generated to contain  
 CC amino acid changes at residues 492-494. (Note - this sequence is not  
 CC given in the specification but is based on the HGF sequence given in  
 CC AAR20005). The generated mutant contains the sequence Lys-Gln-Gly-Arg-  
 CC Val, which replaces the wild type sequence Lys-Glu-Leu-Arg-Val. The HGF  
 CC is translated as single chain protein which is activated to a two chain  
 CC protein by protease cleavage between residues 494-5, producing the alpha  
 CC and beta chains. The novel sequence alters the protease recognition site,  
 CC putatively introducing a Factor Xa recognition site. The novel HGF deriv.  
 CC can be activated specifically at the site of injury in a blood vessel.  
 CC (See AAR87522-5 for different HGF derivs.). The novel HGF derivs. were  
 CC generated by point mutations using the oligonucleotides AAT06762-5  
 XX  
 SQ Sequence 728 AA;

Query Match 99.9%; Score 2601; DB 2; Length 728;  
 Best Local Similarity 99.8%; Pred. No. 9.1e-165;  
 Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERRRRNTIIEFKSAKTTLIKIDPAKIKTKKVNNTADQCANRCTRNKGLPFTCKAVFPDK 60  
 DB 32 QRRRRNTIIEFKSAKTTLIKIDPAKIKTKKVNNTADQCANRCTRNKGLPFTCKAVFPDK 91  
 QY 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKCOP 120  
 DB 92 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKCOP 151  
 QY 121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCEVEVC 180  
 DB 152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCEVEVC 211  
 QY 181 MTCNGSYRGKDLMDHTESGKICORWDHQTPIRHKFLPERYPDKGFDNRYCRNPDGQRPWC 240  
 DB 212 MTCNGSYRGKDLMDHTESGKICORWDHQTPIRHKFLPERYPDKGFDNRYCRNPDGQRPWC 271  
 QY 241 YTLDPHTRWECYAIKTCADNTMNDTVPLETTETCIQOGGEGYRGVTNTIWNIGIPCGRWMS 300  
 DB 272 YTLDPHTRWECYAIKTCADNTMNDTVPLETTETCIQOGGEGYRGVTNTIWNIGIPCGRWMS 331  
 QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGDQC 360  
 DB 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGDQC 391



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 3, 2005, 06:06:02 ; Search time 242.355 Seconds

(without alignments)  
765.639 Million cell updates/sec

Title: US-09-674-377B-1

Perfect score: 2604  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2601	99.9	447	14	US-10-081-309-2
3	2601	99.9	494	18	US-10-926-088A-1
4	2601	99.9	726	17	US-10-872-198-120
5	2601	99.9	726	20	US-11-021-951-120
6	2601	99.9	728	8	US-08-605-221-2
7	2601	99.9	728	16	US-10-813-805-10
8	2601	99.9	728	15	US-10-475-616-2
9	2601	99.9	728	17	US-10-498-333-7
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11	2563.5	98.4	489	18	US-10-926-088A-2

12	2563.5	98.4	723	8	US-08-605-221-4
13	2563.5	98.4	1109	18	US-10-509-247A-20
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ALIGNMENTS

RESULT 1  
US-09-951-629-1  
Sequence 1, Application US/09951629  
Publication No. US20020004480A1  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, Toshikazu  
TITLE OF INVENTION: Anti-Cancer Agent  
FILE REFERENCE: 4373-0101P  
CURRENT APPLICATION NUMBER: US/09/951,629  
CURRENT FILING DATE: 2001-09-14  
PRIOR APPLICATION NUMBER: JP 300728  
PRIOR FILING DATE: 1995-10-24  
PRIOR APPLICATION NUMBER: PCT/J996/03105  
PRIOR FILING DATE: 1996-10-23  
PRIOR APPLICATION NUMBER: US 09/471,032  
PRIOR FILING DATE: 1999-12-23  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 447  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-951-629-1

Query Match  
Best Local Similarity 99.9%; Score 2601; DB 9; Length 447;  
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKKRRNTIHEFKSAKTLTIKIDPAKIKTKKVVNTADQCANRCTRNKGLPFTCKAFVFDK 60  
DB 1 QKKRRNTIHEFKSAKTLTIKIDPAKIKTKKVVNTADQCANRCTRNKGLPFTCKAFVFDK 60  
QY 61 ARKQCIWPFPPNMSGGVKKEFGHEPDLYENKQYIRNCITIGKRSYKGYSTIKSGIKCP 120

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Qy 121 WSSMTPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEYREYECVDPQSEVVC 180
Db 121 WSSMTPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEYREYECVDPQSEVVC 180
Qy 181 MTCNGBSTRGLMDHTESGKICQRMWHQTPHRRKFLPERYPDKGFPDNYCRNPDGQPRPWC 240
Db 181 MTCNGBSTRGLMDHTESGKICQRMWHQTPHRRKFLPERYPDKGFPDNYCRNPDGQPRPWC 240
Qy 241 YTLDPHTHWEYCAIKTCADNTMNDTVPLETTTECLOGGEGYRGVTNTIWMGIPQQRWDS 300
Db 241 YTLDPHTHWEYCAIKTCADNTMNDTVPLETTTECLOGGEGYRGVTNTIWMGIPQQRWDS 300
Qy 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360
Db 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360
Qy 361 YRGNKNYMGUNLSQTRSGLTCSMDKXNEDLHRHIFWEPDASKLNENYCRNPDGDAHGFW 420
Db 361 YRGNKNYMGUNLSQTRSGLTCSMDKXNEDLHRHIFWEPDASKLNENYCRNPDGDAHGFW 420
Qy 421 CYTGNPLIPWDYCPISRCGSDTTPITV 447
Db 421 CYTGNPLIPWDYCPISRCGSDTTPITV 447
```

```
RESULT 2
US-10-081-309-2
; Sequence 2, Application US/10081309
; Publication No. US20030012775A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Peg Conjugates of NK4
; FILE REFERENCE: 20859
; CURRENT APPLICATION NUMBER: US/10/081,309
; CURRENT FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: homosapiens
US-10-081-309-2
```

```
Query Match 99.9%; Score 2601; DB 14; Length 447;
Best Local Similarity 99.8%; Pred. No. 1,1e-211;
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 EKKRRNTIHEFKKSAKTLIKIDPALKIKTKKVNNTADQCANRCTRNKGLPTCKAFVFDK 60
Db 1 EKKRRNTIHEFKKSAKTLIKIDPALKIKTKKVNNTADQCANRCTRNKGLPTCKAFVFDK 60
Qy 61 ARKQCLMPFENSMSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGVSTITKSGIKOP 120
Db 61 ARKQCLMPFENSMSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGVSTITKSGIKOP 120
Qy 121 WSSMTPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEYREYECVDPQSEVVC 180
Db 121 WSSMTPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEYREYECVDPQSEVVC 180
Qy 181 MTCNGBSTRGLMDHTESGKICQRMWHQTPHRRKFLPERYPDKGFPDNYCRNPDGQPRPWC 240
Db 181 MTCNGBSTRGLMDHTESGKICQRMWHQTPHRRKFLPERYPDKGFPDNYCRNPDGQPRPWC 240
Qy 241 YTLDPHTHWEYCAIKTCADNTMNDTVPLETTTECLOGGEGYRGVTNTIWMGIPQQRWDS 300
Db 241 YTLDPHTHWEYCAIKTCADNTMNDTVPLETTTECLOGGEGYRGVTNTIWMGIPQQRWDS 300
Qy 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360
Db 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360
Qy 361 YRGNKNYMGUNLSQTRSGLTCSMDKXNEDLHRHIFWEPDASKLNENYCRNPDGDAHGFW 420
Db 361 YRGNKNYMGUNLSQTRSGLTCSMDKXNEDLHRHIFWEPDASKLNENYCRNPDGDAHGFW 420
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Qy 361 YRGNKNYMGUNLSQTRSGLTCSMDKXNEDLHRHIFWEPDASKLNENYCRNPDGDAHGFW 420
Db 361 YRGNKNYMGUNLSQTRSGLTCSMDKXNEDLHRHIFWEPDASKLNENYCRNPDGDAHGFW 420
Qy 421 CYTGNPLIPWDYCPISRCGSDTTPITV 447
Db 421 CYTGNPLIPWDYCPISRCGSDTTPITV 447
```

```
RESULT 3
US-10-926-088A-1
; Sequence 1, Application US/10926088A
; Publication No. US20050164918A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA Toshikazu
; APPLICANT: MATSUMOTO Kunio
; APPLICANT: FUKUTA Kazuhito
; TITLE OF INVENTION: A segment of glycosylation-deficient HGF alpha-chain
; FILE REFERENCE: 2004-13284/W/C/01736
; CURRENT APPLICATION NUMBER: US/10/926,088A
; CURRENT FILING DATE: 2004-08-26
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: alpha-chain of human hepatocyte growth factor
US-10-926-088A-1
```

```
Query Match 99.9%; Score 2601; DB 18; Length 494;
Best Local Similarity 99.8%; Pred. No. 1,3e-211;
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 EKKRRNTIHEFKKSAKTLIKIDPALKIKTKKVNNTADQCANRCTRNKGLPTCKAFVFDK 60
Db 32 EKKRRNTIHEFKKSAKTLIKIDPALKIKTKKVNNTADQCANRCTRNKGLPTCKAFVFDK 91
Qy 61 ARKQCLMPFENSMSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGVSTITKSGIKOP 120
Db 92 ARKQCLMPFENSMSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGVSTITKSGIKOP 151
Qy 121 WSSMTPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEYREYECVDPQSEVVC 180
Db 152 WSSMTPHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCTSNPEYREYECVDPQSEVVC 211
Qy 181 MTCNGBSTRGLMDHTESGKICQRMWHQTPHRRKFLPERYPDKGFPDNYCRNPDGQPRPWC 240
Db 212 MTCNGBSTRGLMDHTESGKICQRMWHQTPHRRKFLPERYPDKGFPDNYCRNPDGQPRPWC 271
Qy 241 YTLDPHTHWEYCAIKTCADNTMNDTVPLETTTECLOGGEGYRGVTNTIWMGIPQQRWDS 300
Db 272 YTLDPHTHWEYCAIKTCADNTMNDTVPLETTTECLOGGEGYRGVTNTIWMGIPQQRWDS 331
Qy 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360
Db 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 391
Qy 361 YRGNKNYMGUNLSQTRSGLTCSMDKXNEDLHRHIFWEPDASKLNENYCRNPDGDAHGFW 420
Db 392 YRGNKNYMGUNLSQTRSGLTCSMDKXNEDLHRHIFWEPDASKLNENYCRNPDGDAHGFW 451
Qy 421 CYTGNPLIPWDYCPISRCGSDTTPITV 447
Db 452 CYTGNPLIPWDYCPISRCGSDTTPITV 478
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```
RESULT 4
US-10-872-198-120
; Sequence 120, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
```



```

; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOTSMERER
; APPLICANT: Ulrich Ketting
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000204
; CURRENT APPLICATION NUMBER: US/10/872.198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-120

```

Query Match 99.9%; Score 2601; DB 17; Length 726;

Best Local Similarity 99.8%; Pred. No. 2e-211; Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ERRKRRYTHIEFKSAAKTLIKIDPALKIKTKKNTADQCANRCTRNGKLPFTCKAFVFDK 60
   :
DB 30 QRRRRYTHIEFKSAAKTLIKIDPALKIKTKKNTADQCANRCTRNGKLPFTCKAFVFDK 89
   :
QY 61 ARKQCLMPFPNSMSGVKEFGHEFDLYENKDYIRNCIIGKGSYKGTVAITSIGIKCP 120
   :
DB 90 ARKQCLMPFPNSMSGVKEFGHEFDLYENKDYIRNCIIGKGSYKGTVAITSIGIKCP 149
   :
QY 121 WSSMIDPHEHSFLPSSYRGKDLQENYCRNPDGEGGWCFTSNDEVRVEVCDIPQCEVEEC 180
   :
DB 150 WSSMIDPHEHSFLPSSYRGKDLQENYCRNPDGEGGWCFTSNDEVRVEVCDIPQCEVEEC 209
   :
QY 181 MTCNGSSYRGKDLMDHTSSGKICQRMWDQTPHRRKFLPERYPDKGFDNNYCRNPDGQRRPWC 240
   :
DB 210 MTCNGSSYRGKDLMDHTSSGKICQRMWDQTPHRRKFLPERYPDKGFDNNYCRNPDGQRRPWC 269
   :
QY 241 YTLDPHTRMVEYCAIKTCADNTMNDTVPLETTETCIGQSGYRGYVNTIWNGLPCQRMDS 300
   :
DB 270 YTLDPHTRMVEYCAIKTCADNTMNDTVPLETTETCIGQSGYRGYVNTIWNGLPCQRMDS 329
   :
QY 301 QYHEHDMTPENKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360
   :
DB 330 QYHEHDMTPENKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 389
   :
QY 361 YRNGKNYVGNLSQTSRSGLTCSMWDKMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 420
   :
DB 390 YRNGKNYVGNLSQTSRSGLTCSMWDKMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 449
   :
QY 421 CYTGNPLIPMDYCPISRCGEGDTPTIV 447
   :
DB 450 CYTGNPLIPMDYCPISRCGEGDTPTIV 476

```

RESULT 5  
US-11-021-951-120

; Sequence 120, Application US/11021951  
; Publication No. US20050175581A1  
; GENERAL INFORMATION:  
; APPLICANT: HAUPTS, Ulrich  
; APPLICANT: KOLTERMANN, Andre  
; APPLICANT: SCHEIDIG, Andreas

```

; APPLICANT: VOTSMERER, Christian
; APPLICANT: Ketting, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; FILE REFERENCE: 04156.000205
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-120

```

Query Match 99.9%; Score 2601; DB 20; Length 726;

Best Local Similarity 99.8%; Pred. No. 2e-211; Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ERRKRRYTHIEFKSAAKTLIKIDPALKIKTKKNTADQCANRCTRNGKLPFTCKAFVFDK 60
   :
DB 30 QRRRRYTHIEFKSAAKTLIKIDPALKIKTKKNTADQCANRCTRNGKLPFTCKAFVFDK 89
   :
QY 61 ARKQCLMPFPNSMSGVKEFGHEFDLYENKDYIRNCIIGKGSYKGTVAITSIGIKCP 120
   :
DB 90 ARKQCLMPFPNSMSGVKEFGHEFDLYENKDYIRNCIIGKGSYKGTVAITSIGIKCP 149
   :
QY 121 WSSMIDPHEHSFLPSSYRGKDLQENYCRNPDGEGGWCFTSNDEVRVEVCDIPQCEVEEC 180
   :
DB 150 WSSMIDPHEHSFLPSSYRGKDLQENYCRNPDGEGGWCFTSNDEVRVEVCDIPQCEVEEC 209
   :
QY 181 MTCNGSSYRGKDLMDHTSSGKICQRMWDQTPHRRKFLPERYPDKGFDNNYCRNPDGQRRPWC 240
   :
DB 210 MTCNGSSYRGKDLMDHTSSGKICQRMWDQTPHRRKFLPERYPDKGFDNNYCRNPDGQRRPWC 269
   :
QY 241 YTLDPHTRMVEYCAIKTCADNTMNDTVPLETTETCIGQSGYRGYVNTIWNGLPCQRMDS 300
   :
DB 270 YTLDPHTRMVEYCAIKTCADNTMNDTVPLETTETCIGQSGYRGYVNTIWNGLPCQRMDS 329
   :
QY 301 QYHEHDMTPENKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360
   :
DB 330 QYHEHDMTPENKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 389
   :
QY 361 YRNGKNYVGNLSQTSRSGLTCSMWDKMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 420
   :
DB 390 YRNGKNYVGNLSQTSRSGLTCSMWDKMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 449
   :
QY 421 CYTGNPLIPMDYCPISRCGEGDTPTIV 447
   :
DB 450 CYTGNPLIPMDYCPISRCGEGDTPTIV 476

```

RESULT 6

US-08-605-221-2  
; Sequence 2, Application US/08605221  
; Publication No. US20030060403A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, Toshikazu

```

: TITLE OR INVENTION: THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE
: FILE REFERENCE: 2520-0101P
: CURRENT APPLICATION NUMBER: US/08/605,221
: CURRENT FILING DATE: 1996-03-15
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 728
: TYPE: PRT
: ORGANISM: Homo sapiens
: OTHER INFORMATION: HGF-A (Full length HGF)
: JS-08-605-221-2

```

Query Match	99.9%	Score 2601;	DB 8;	Length 728;
Best Local Similarity	99.8%;	Pred. No. 2e-211;		
Matches 446;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	ERKRKNNTTHEFFKSAKTTLLIKIDPAKIKTKKVTADOCANRCTRKKGJLFTCKAFVFDK	60
Db	32	QKRKNNTTHEFFKSAKTTLLIKIDPAKIKTKKVTADOCANRCTRKKGJLFTCKAFVFDK	91
Qy	61	ARKQCLWPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVASITYSKIGKOP	120
Db	92	ARKQCLWPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVASITYSKIGKOP	151
Qy	121	WSSMTLPHHSFLPSSYRGKDOENYCRNRRGEGGGMWCFPSNBEVRYEVDIDQCSEVEC	180
Db	152	WSSMTLPHHSFLPSSYRGKDOENYCRNRRGEGGGMWCFPSNBEVRYEVDIDQCSEVEC	211
Qy	181	MTCNSESRYGLMDHTESGKICORMDHQTPHRRKFLPERYDCKFDDNYCENPDCGPRPWC	240
Db	212	MTCNSESRYGLMDHTESGKICORMDHQTPHRRKFLPERYDCKFDDNYCENPDCGPRPWC	271
Qy	241	YTLDPHTMEYCAIKTCADNTMNDTDVPLETTECICOGGEGYRGVTNTIINGJPCORWDS	300
Db	272	YTLDPHTMEYCAIKTCADNTMNDTDVPLETTECICOGGEGYRGVTNTIINGJPCORWDS	331
Qy	301	QYPHEHDMPEMFKCDLRENYCRNPDGSSPMCFPTDPPIRIGVCSQIPNCMSHQDC	366
Db	332	QYPHEHDMPEMFKCDLRENYCRNPDGSSPMCFPTDPPIRIGVCSQIPNCMSHQDC	391
Qy	361	YRGNGKNVYGNLSQTRSGLTCSWMDXNMBDLHRHIFWEPDASKLNNYCNCPDDDAHGPW	420
Db	392	YRGNGKNVYGNLSQTRSGLTCSWMDXNMBDLHRHIFWEPDASKLNNYCNCPDDDAHGPW	451
Qy	421	CYTGNDPLIPWDYCPISRCBGDTPTTV 447	
Db	452	CYTGNDPLIPWDYCPISRCBGDTPTTV 478	

```

RESULT 7
US-10-813-805-10
; Sequence 10, Application US/108133805
; Publication No. US20040191902A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER INC.
; APPLICANT: Hambr, John E.
; APPLICANT: Roach, Marsha L.
; TITLE OF INVENTION: GROWTH AND DIFFERENTIATION OF STEM CELLS
; FILE REFERENCE: PC25028A
; CURRENT APPLICATION NUMBER: US/10/813,805
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US 60/459,449
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO. 10
; LENGTH: 728
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-813-805-10

```

Query Match 99.9%; Score 2601; DB 16; Length 728;

Best Local Similarity	99.8%	Pred. No.	2e-211
Matches	446	Conservative	1
		Mismatches	0
		Indels	0
		Gaps	0

QY	1	ORRRRNTTHERFFKSKTLLIKIDPALKITKTKVNTADOCANCTRNGKJLPFTCKAFVPRK	60
Db	32	ORRRRNTTHERFFKSKTLLIKIDPALKITKTKVNTADOCANCTRNGKJLPFTCKAFVPRK	91
QY	61	ARKOCLMFPFMSMSGVKKFEGHEFDLYENKDYINNCIIIGKRSYKGVSIITKSGIKCOP	120
Db	92	ARKOCLMFPFMSMSGVKKFEGHEFDLYENKDYINNCIIIGKRSYKGVSIITKSGIKCOP	151
QY	121	WSSMTPIHHSHFLPSSYRGKDLOENYCRNPDGEGGPMCTSNPEVRYEVCDDIPQCEVBC	180
Db	152	WSSMTPIHHSHFLPSSYRGKDLOENYCRNPDGEGGPMCTSNPEVRYEVCDDIPQCEVBC	211
QY	181	MTCNSESRYGLMDHTESGKICORWHDQPHRHKFLPERYPDGCFPDNYCRNPDGQRPWC	240
Db	212	MTCNSESRYGLMDHTESGKICORWHDQPHRHKFLPERYPDGCFPDNYCRNPDGQRPWC	271
QY	241	YTLDPHTRWECALITCADNTMNDTDPVLETTETCIGOGGEGRYGVNTIWNIGPCORWMS	300
Db	272	YTLDPHTRWECALITCADNTMNDTDPVLETTETCIGOGGEGRYGVNTIWNIGPCORWMS	331
QY	301	OYPEHDMTPENFKCKDLRENYCRNPDGSESFWCFTTDINIRVGYCSQIPNCDMSHGQDC	360
Db	332	OYPEHDMTPENFKCKDLRENYCRNPDGSESFWCFTTDINIRVGYCSQIPNCDMSHGQDC	391
QY	361	YRGNGKNYMGNLISQTRSGITCSMDWKNMEDLHRHIFWEBDASKLNNYCRNPDDDAHGFW	420
Db	392	YRGNGKNYMGNLISQTRSGITCSMDWKNMEDLHRHIFWEBDASKLNNYCRNPDDDAHGFW	451
QY	421	CYTGNPFLIPWDCYPISRCEGDTTPITIV	447
Db	452	CYTGNPFLIPWDCYPISRCEGDTTPITIV	478

```

RESULT 8
US-10-475-616-2
; Sequence 2, Application US/10475616
; Publication No. US20040236073A1
; GENERAL INFORMATION:
; APPLICANT: Cherardi, Ermanno
; APPLICANT: Iisetha, Daniel
; APPLICANT: Blundell, Thomas L
; APPLICANT: Chirgadze, Dmitry Y
; TITLE OF INVENTION: The NK1 Fragment of Hepatocyte Growth Factor/Scatter
; TITLE OF INVENTION: Factor (HGF/SF) and Variants thereof, and Their Use
; FILE REFERENCE: 2502489-991180
; CURRENT APPLICATION NUMBER: US/10/475,616
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: PCT/GB02/01941
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: GB 011430.6
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-475-616-2

```

Query Match	99.9%	Score 2601;	DB 16;	Length 728;
Best Local Similarity	99.8%	Pred. No. 2e-211;		
Matches 446;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 EKKRRNTTIEFFKSKATTLIKIDPALPKITKRVNADOCANCTRRNGKLPFTCKAAVFDK 60  
Db 32 QKRRNTTIEFFKSKATTLIKIDPAKIKTKRVNADOCANCTRRNGKLPFTCKAAVFDK 91  
QY 61 AKKCIAMPEFNSMSGGVKKEFGHEFDLVENKDYIRNCIIIGKGRSVYKTVSITKSGIKCP 120  
Db 92 AKKCIAMPEFNSMSGGVKKEFGHEFDLVENKDYIRNCIIIGKGRSVYKTVSITKSGIKCP 151

QY 121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCTSNBEVYEVCDIPQCSVEVC 180  
 DB 152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCTSNBEVYEVCDIPQCSVEVC 211  
 QY 181 MTCNGSYRGKDLMDHTSSGKICQWHDQTPHRAKFLPERYPDKGFDNNYCRNPDGQRPWC 240  
 DB 212 MTCNGSYRGKDLMDHTSSGKICQWHDQTPHRAKFLPERYPDKGFDNNYCRNPDGQRPWC 271  
 QY 241 YLDPHTRWECYCAIKTCADNTMNDTVPLETTTCIOGQEGYRGVTNTWNGIPQCRWMS 300  
 DB 272 YLDPHTRWECYCAIKTCADNTMNDTVPLETTTCIOGQEGYRGVTNTWNGIPQCRWMS 331  
 QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
 DB 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 391  
 QY 361 YRGNGKNYMGNTSQTSSGLTCSMDKXMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 420  
 DB 392 YRGNGKNYMGNTSQTSSGLTCSMDKXMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 451  
 QY 421 CYTGNPLIPWDYCPISRCBGDTTPTIV 447  
 DB 452 CYTGNPLIPWDYCPISRCBGDTTPTIV 478

RESULT 9

US-10-498-332-7  
 ; Sequence 7, Application US/10498332  
 ; Publication No. US20050113284A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nakamura, Motono  
 ; APPLICANT: Higuchi, Toshio  
 ; APPLICANT: Yamasaki, Yoshiki  
 ; APPLICANT: Orita, Takuya  
 ; TITLE OF INVENTION: PHARMACEUTICAL AGENTS AND METHODS FOR  
 ; FILE REFERENCE: 14539-016US1  
 ; CURRENT APPLICATION NUMBER: US/10/498,332  
 ; CURRENT FILING DATE: 2004-06-11  
 ; PRIOR APPLICATION NUMBER: PCT/JP02/13014  
 ; PRIOR FILING DATE: 2002-12-12  
 ; PRIOR APPLICATION NUMBER: JP 2002-352924  
 ; PRIOR FILING DATE: 2002-12-04  
 ; PRIOR APPLICATION NUMBER: JP 2001-380158  
 ; PRIOR FILING DATE: 2001-12-13  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 728  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-498-332-7

Query Match 99.9%; Score 2601; DB 17; Length 728;  
 Best Local Similarity 99.8%; Pred. No. 2e-211;  
 Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKKRRNTIHEFKSATTLLIKIDPALKITKKNVTADQCANRCTRNKGLPFTCKAVFPA 60  
 DB 32 ORRRRTIHEFKSATTLLIKIDPALKITKKNVTADQCANRCTRNKGLPFTCKAVFPA 91  
 QY 61 ARKQCLMPFPNSMSGVKKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITSGIKQCP 120  
 DB 92 ARKQCLMPFPNSMSGVKKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITSGIKQCP 151  
 QY 121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCTSNBEVYEVCDIPQCSVEVC 180  
 DB 152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCTSNBEVYEVCDIPQCSVEVC 211  
 QY 181 MTCNGSYRGKDLMDHTSSGKICQWHDQTPHRAKFLPERYPDKGFDNNYCRNPDGQRPWC 240  
 DB 212 MTCNGSYRGKDLMDHTSSGKICQWHDQTPHRAKFLPERYPDKGFDNNYCRNPDGQRPWC 271

QY 241 YLDPHTRWECYCAIKTCADNTMNDTVPLETTTCIOGQEGYRGVTNTWNGIPQCRWMS 300  
 DB 272 YLDPHTRWECYCAIKTCADNTMNDTVPLETTTCIOGQEGYRGVTNTWNGIPQCRWMS 331  
 QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
 DB 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 391  
 QY 361 YRGNGKNYMGNTSQTSSGLTCSMDKXMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 420  
 DB 392 YRGNGKNYMGNTSQTSSGLTCSMDKXMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 451  
 QY 421 CYTGNPLIPWDYCPISRCBGDTTPTIV 447  
 DB 452 CYTGNPLIPWDYCPISRCBGDTTPTIV 478

RESULT 10

US-10-149-103A-1  
 ; Sequence 1, Application US/10149103A  
 ; Publication No. US20040121945A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liang, Hong  
 ; APPLICANT: Sim, Kim Lee  
 ; APPLICANT: Day, Clara  
 ; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer  
 ; FILE REFERENCE: 05213-0592 43170-274540  
 ; CURRENT APPLICATION NUMBER: US/10/149,103A  
 ; CURRENT FILING DATE: 2003-05-06  
 ; PRIOR APPLICATION NUMBER: PCT/US00/34039  
 ; PRIOR FILING DATE: 2000-12-15  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 727  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-149-103A-1

Query Match 98.5%; Score 2565; DB 16; Length 727;  
 Best Local Similarity 98.2%; Pred. No. 2.3e-208;  
 Matches 438; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKKRRNTIHEFKSATTLLIKIDPALKITKKNVTADQCANRCTRNKGLPFTCKAVFPA 61  
 DB 33 KRRRTIHEFKSATTLLIKIDPALKITKKNVTADQCANRCTRNKGLPFTCKAVFPA 92  
 QY 62 RKQCLMPFPNSMSGVKKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITSGIKQCP 121  
 DB 93 RKQCLMPFPNSMSGVKKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITSGIKQCP 152  
 QY 122 SSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCTSNBEVYEVCDIPQCSVEVC 181  
 DB 153 SSMIPHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCTSNBEVYEVCDIPQCSVEVC 212  
 QY 182 TONGSYRGKDLMDHTSSGKICQWHDQTPHRAKFLPERYPDKGFDNNYCRNPDGQRPWC 241  
 DB 213 TONGSYRGKDLMDHTSSGKICQWHDQTPHRAKFLPERYPDKGFDNNYCRNPDGQRPWC 272  
 QY 242 YLDPHTRWECYCAIKTCADNTMNDTVPLETTTCIOGQEGYRGVTNTWNGIPQCRWMS 301  
 DB 273 YLDPHTRWECYCAIKTCADNTMNDTVPLETTTCIOGQEGYRGVTNTWNGIPQCRWMS 332  
 QY 302 YHHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 361  
 DB 333 YHHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 392  
 QY 362 RGNKKNYMGNTSQTSSGLTCSMDKXMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 421  
 DB 393 RGNKKNYMGNTSQTSSGLTCSMDKXMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 452  
 QY 422 YTGNNPLIPWDYCPISRCBGDTTPTIV 447

Db 453 YTGNDPLIPMDYCPISRCGDDTPTIV 478

RESULT 11

US-10-926-088A-2

Sequence 2, Application US/10926088A

Publication No. US20050164918A1

GENERAL INFORMATION:

APPLICANT: NAKAMURA Toshikazu

APPLICANT: MATSUMOTO Kunio

APPLICANT: FUKUTA Kazuhito

TITLE OF INVENTION: A segment of glycosylation-deficient HGF alpha-chain

FILE REFERENCE: 2004-1328A/MMC/01736

CURRENT APPLICATION NUMBER: US/10/926,088A

CURRENT FILING DATE: 2004-08-26

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 2

LENGTH: 489

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE:

OTHER INFORMATION: alpha-chain of human hepatocyte growth factor of five amino acid-

US-10-926-088A-2

Query Match 98.4%; Score 2563.5; DB 18; Length 489;

Best Local Similarity 98.7%; Pred. No. 1.9e-208;

Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 ERKRRNTIHEFKSAKTLIKIDPALKIKTKVNTADOCANRCTRNKGLPFTCKAFVFDK 60

Db 32 QRKRRTIHEFKSAKTLIKIDPALKIKTKVNTADOCANRCTRNKGLPFTCKAFVFDK 91

QY 61 ARKQCLWPFNSMSGVKKFEGHEFDLYENKDIYRNCIIIGKRSYKGVSTIKSGIKOP 120

Db 92 ARKQCLWPFNSMSGVKKFEGHEFDLYENKDIYRNCIIIGKRSYKGVSTIKSGIKOP 151

QY 121 WSMIPIHEHFLPSSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVEC 180

Db 152 WSMIPIHEHFLPSSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVEC 206

QY 161 MTCNGESYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVEC 240

Db 207 MTCNGESYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVEC 266

QY 241 YTLDPHTREWCALIKTCADNTMNDTVDVPLETTECIQOGEGYRGVNTIWMGICQWRWS 300

Db 267 YTLDPHTREWCALIKTCADNTMNDTVDVPLETTECIQOGEGYRGVNTIWMGICQWRWS 326

QY 301 QYRPHEDMTPEPFCKDLRENYCRNPDGSESPMCFSTNPEVRYEVCDIPOCSEVEC 360

Db 327 QYRPHEDMTPEPFCKDLRENYCRNPDGSESPMCFSTNPEVRYEVCDIPOCSEVEC 386

QY 361 YRNGKNYMGSLQTRSGILTCSMWDMKMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 420

Db 387 YRNGKNYMGSLQTRSGILTCSMWDMKMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 446

QY 421 CYTGNPLIPMDYCPISRCGDDTPTIV 447

Db 447 CYTGNPLIPMDYCPISRCGDDTPTIV 473

RESULT 12

US-08-605-221-4

Sequence 4, Application US/08605221

Publication No. US20030060403A1

GENERAL INFORMATION:

APPLICANT: NAKAMURA, Toshikazu

TITLE OF INVENTION: THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE

FILE REFERENCE: 2520-0101P

CURRENT APPLICATION NUMBER: US/08/605,221

CURRENT FILING DATE: 1996-03-15

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 723

TYPE: PRT

ORGANISM: Homo sapiens

OTHER INFORMATION: HGF-B (five amino acids deletion type)

US-08-605-221-4

Query Match 98.4%; Score 2563.5; DB 8; Length 723;

Best Local Similarity 98.7%; Pred. No. 3e-208;

Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 ERKRRNTIHEFKSAKTLIKIDPALKIKTKVNTADOCANRCTRNKGLPFTCKAFVFDK 60

Db 32 QRKRRTIHEFKSAKTLIKIDPALKIKTKVNTADOCANRCTRNKGLPFTCKAFVFDK 91

QY 61 ARKQCLWPFNSMSGVKKFEGHEFDLYENKDIYRNCIIIGKRSYKGVSTIKSGIKOP 120

Db 92 ARKQCLWPFNSMSGVKKFEGHEFDLYENKDIYRNCIIIGKRSYKGVSTIKSGIKOP 151

QY 121 WSMIPIHEHFLPSSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVEC 180

Db 152 WSMIPIHEHFLPSSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVEC 206

QY 181 MTCNGESYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVEC 240

Db 207 MTCNGESYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVEC 266

QY 241 YTLDPHTREWCALIKTCADNTMNDTVDVPLETTECIQOGEGYRGVNTIWMGICQWRWS 300

Db 267 YTLDPHTREWCALIKTCADNTMNDTVDVPLETTECIQOGEGYRGVNTIWMGICQWRWS 326

QY 301 QYRPHEDMTPEPFCKDLRENYCRNPDGSESPMCFSTNPEVRYEVCDIPOCSEVEC 360

Db 327 QYRPHEDMTPEPFCKDLRENYCRNPDGSESPMCFSTNPEVRYEVCDIPOCSEVEC 386

QY 361 YRNGKNYMGSLQTRSGILTCSMWDMKMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 420

Db 387 YRNGKNYMGSLQTRSGILTCSMWDMKMDLHRHIFWEPDASKLNNYCRNPDGDAHGPW 446

QY 421 CYTGNPLIPMDYCPISRCGDDTPTIV 447

Db 447 CYTGNPLIPMDYCPISRCGDDTPTIV 473

RESULT 13

US-10-509-247A-20

Sequence 20, Application US/10509247A

Publication No. US20050181064A1

GENERAL INFORMATION:

APPLICANT: Japan Science and Technology Corporation

APPLICANT: Kuroda, Shunichi

APPLICANT: Tanizawa, Katsuyuki

APPLICANT: Kondo, Akihiko

APPLICANT: Ueda, Masakazu

APPLICANT: Sano, Masaharu

APPLICANT: Tada, Hiroko

TITLE OF INVENTION: DRUG CONTAINING HOLLOW PROTEIN NANOPARTICLES OF PARTICLE-FORMING

FILE REFERENCE: P023P01/US

CURRENT APPLICATION NUMBER: US/10/509,247A

CURRENT FILING DATE: 2004-09-28

PRIOR APPLICATION NUMBER: PCT/JP03/02602

PRIOR FILING DATE: 2003-03-05

PRIOR APPLICATION NUMBER: JP2002-97280

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.3

SEQ ID NO 20

LENGTH: 1109

TYPE: PRT

ORGANISM: Artificial Sequence

```

;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-509-247A-20

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Query Match	98.4%;	Score 2563.5;	DB 18;	Length 1109;
Best Total Similarity	99.7%;	Score 2563.5;	DB 18;	Length 1109;

QY	1	ERGRRTTIEHFKSATTTLIKIDPLAKITKXKVNTADOCARCTRNGLPETCAFAVEDK	60
Db	418	QRGRRTTIEHFKSATTTLIKIDPLAKITKXKVNTADOCARCTRNGLPETCAFAVEDK	4777
QY	61	ARKOCILMPPNSSGVCKEFGHEFDLYENKDIYINCIIGKRSYKGVSTITSKGIKOP	120
Db	478	ARKOCILMPPNSSGVCKEFGHEFDLYENKDIYINCIIGKRSYKGVSTITSKGIKOP	537
QY	121	WSKMIIEHSPILBSSYRGKIOENYCRNPDGEGPWCFTSNPEYRYEVDIPQCSVEEC	180
Db	538	WSKMIIEHSPILBSSYRGKIOENYCRNPDGEGPWCFTSNPEYRYEVDIPQCSVEEC	592
QY	181	MTCNGESYRGLMDHTESGKICORMWQHPHRHKFLPERYPRKGFDDNYCRNPDQPRPMC	240
Db	593	MTCNGESYRGLMDHTESGKICORMWQHPHRHKFLPERYPRKGFDDNYCRNPDQPRPMC	652
QY	241	YTIIDPHTREYCAIKTCADNTMNDVPLETTECIQGGSGYRGTVANTWNGIPQQRWDS	300
Db	653	YTIIDPHTREYCAIKTCADNTMNDVPLETTECIQGGSGYRGTVANTWNGIPQQRWDS	712
QY	301	QYEHEDMTPENPKCKDLRENYCRNPDGSESPWCTTDPNIRVYCGSOIPNCOMSHODC	360
Db	713	QYEHEDMTPENPKCKDLRENYCRNPDGSESPWCTTDPNIRVYCGSOIPNCOMSHODC	772
QY	361	YRNGNGXNYGNLSQTRSGLTCSMDNMKNEDLHRHIFWEPDASKUNENYCRNPDDAHGPW	420
Db	773	YRNGNGXNYGNLSQTRSGLTCSMDNMKNEDLHRHIFWEPDASKUNENYCRNPDDAHGPW	832
QY	421	CYTGNPILIPWDYCPISRCRGDTTPPV 447	
Db	833	CYTGNPILIPWDYCPISRCRGDTTPPV 859	

RESULT 14  
US-10-133-912-18  
Sequence 18, Application US/10133912  
Publication No. US20020165356A1  
GENERAL INFORMATION:  
APPLICANT: Kinosaki, Masahiko  
Yamaguchi, Kyoji  
Goto, Masaaki  
Murakami, Akihiko  
Ueda, Masatsugu  
Higashio, Kanji  
Yamashita, Yasushi  
TITLE OF INVENTION: TCF MUTANT  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burgeess, Ryan and Wayne  
STREET: 370 Lexington Avenue, Suite 2105  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 10017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/5 inch diskette  
COMPUTER: PC's LIMITED SYSTEM 200  
OPERATING SYSTEM: WORD FOR WINDOWS  
SOFTWARE: MICROSOFT WINDOWS 98  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/0133,912  
FILING DATE: 25-Apr-2002  
CLASSIFICATION: <UNKNOWN>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,519

? FILING DATE: 26-Aug-1996  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Wayne, Milton J.  
 ? REGISTRATION NUMBER: 17,906  
 ? REFERENCE/DOCKET NUMBER: U-Wp-5240PCT  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: 212-683-8150  
 ? TELEFAX: 212-532-4285  
 ? INFORMATION FOR SEQ ID NO: 18:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 723  
 ? TYPE: AMINO ACID  
 ? STRANDEDNESS: SINGLE  
 ? TOPOLOGY: LINEAR  
 ? SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
 ? US-10-133-912-18

Query Match	97.6%;	Score 2541.5;	DB 13;	Length 723;
Best Local Similarity	98.9%;	Pred. No. 2.2e-206;		
Matches 437;	Conservative 0;	Mismatches 0;	Indels 5;	Gaps 1

Qy	6	NTIHEKKSAAKTTLLKIDBALKI	KTKKVNTADOCANCRANKGLPFTCAVFPKAKQC	65
Db	37	NTIHEKKSAAKTTLLKIDBALKI	KTKKVNTADOCANCRANKGLPFTCAVFPKAKQC	96
Qy	66	LMFPNSMSGYKKEFGHEFDL	YENKDYIRNCITIGKGSYGYTSITKSGTICOPSSMI	125
Db	97	LMFPNSMSGYKKEFGHEFDL	YENKDYIRNCITIGKGSYGYTSITKSGTICOPSSMI	156
Qy	126	PHEHSLPSSYKGLQENYCNRP	GGSGPWCFTSNBEVAYEVCDDPQSEVBCMTNG	189
Db	157	PHEHSLPSSYKGLQENYCNRP	GGSGPWCFTSNBEVAYEVCDDPQSEVBCMTNG	211
Qy	186	ESYRGLMDHTESGKICORWDH	OTPRHAKFLPERYPDKGFDNRCRNPDOGRPMCYTLDP	245
Db	212	ESYRGLMDHTESGKICORWDH	OTPRHAKFLPERYPDKGFDNRCRNPDOGRPMCYTLDP	271
Qy	246	HTRWECALKTADNTMNDTVP	LETTCITIGQGGBYRGVNTIINNGICQRMNSOYRPH	305
Db	272	HTRWECALKTADNTMNDTVP	LETTCITIGQGGBYRGVNTIINNGICQRMNSOYRPH	331
Qy	306	HDMTPENFCXDLRENYCRNP	DGSESPPMCFITTDPIRIGYCSQIPNCDSHGQDCYRNG	365
Db	332	HDMTPENFCXDLRENYCRNP	DGSESPPMCFITTDPIRIGYCSQIPNCDSHGQDCYRNG	391
Qy	366	KNYMGNLSQTRSGLTCSMWD	KXMBDLHRIHFWBPDAKXLENYCRNPDDDAHGWCTGN	425
Db	392	KNYMGNLSQTRSGLTCSMWD	KXMBDLHRIHFWBPDAKXLENYCRNPDDDAHGWCTGN	451
Qy	426	PLIPMDYCPISRCBGDTTP	PIV 447	
Db	452	PLIPMDYCPISRCBGDTTP	PIV 473	

RESULT 15  
US-10-133-912-19  
Sequence 19, Application US/10133912  
Publication No. US2002016538A1  
GENERAL INFORMATION:  
APPLICANT: Kinoshaki, Masahiko  
Yamaguchi, Kyoji  
Goto, Masaaki  
Murakami, Akihiko  
Ueda, Masatsugu  
Higashio, Kanji  
Yamashita, Yasushi  
TITLE OF INVENTION: TCF MUTANT  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burgess, Ryan and Wayne  
STREET: 370 Lexington Avenue, Suite 2105  
CITY: NEW YORK  
STATE: NEW YORK

COUNTRY: UNITED STATES OF AMERICA  
ZIP: 10017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/5 inch diskette  
COMPUTER: PC'S LIMITED SYSTEM 200  
OPERATING SYSTEM: WORD FOR WINDOWS  
SOFTWARE: MICROSOFT WINDOWS 98  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/133,912  
FILING DATE: 25-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,519  
FILING DATE: 26-Aug-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mayne, Milton J.  
REGISTRATION NUMBER: 17,906  
REFERENCE/DOCKET NUMBER: U-WP-5240PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-683-8150  
TELEFAX: 212-532-4285  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723  
TYPE: AMINO ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-10-133-912-19  
Query Match 97.5%; Score 2539.5; DB 13; Length 723;  
Best Local Similarity 97.8%; Pred. No. 3.2e-206;  
Matches 437; Conservative 1; Mismatches 4; Indels 5; Gaps 1;  
QY 1 EKKRRNTHEFKSAKTLIKIDPALKIKTKKVNADOCANRCTRNKGLPTCKAFVFDK 60  
DB 32 QRRKRRNTHEFKSAKTLIKIDPALAATAVAVNTADOCANRCTRNKGLPTCKAFVFDK 91  
QY 61 ARKQCLMPFPNMSGVKKFEGHEFDLYENKDYIRNCIIGKRSYKGTVISITKSGIKCP 120  
DB 92 ARKQCLMPFPNMSGVKKFEGHEFDLYENKDYIRNCIIGKRSYKGTVISITKSGIKCP 151  
QY 121 WSSMTIPEHSLPSSYRGKLOENYCRNPRGEGGFWCTSNPEVRYEYCDIPQCEVEEC 180  
DB 152 WSSMTIPEHSLPSSYRGKLOENYCRNPRGEGGFWCTSNPEVRYEYCDIPQCEVEEC 206  
QY 181 MTCNSESYSGLMDHTESGKICQRMHQTHRHKFLPERYPDKGPDNVCRNPDGQPRPWC 240  
DB 207 MTCNSESYSGLMDHTESGKICQRMHQTHRHKFLPERYPDKGPDNVCRNPDGQPRPWC 266  
QY 241 YLDPHTRWYCAIKTCADNTMNDVDVPLETTECTIOGQEGYRGTVNTIWMGI PCQRWDS 300  
DB 267 YLDPHTRWYCAIKTCADNTMNDVDVPLETTECTIOGQEGYRGTVNTIWMGI PCQRWDS 326  
QY 301 QYPHEHDMTPENFKCKDLRENTCRNPDGSESPWCFTTDPNIRVYCSQIPNCDSHGQDC 360  
DB 327 QYPHEHDMTPENFKCKDLRENTCRNPDGSESPWCFTTDPNIRVYCSQIPNCDSHGQDC 386  
QY 361 YRNGNGNVMNLSQRTSSGLTCSMMDKNMMDLHRHIFWEPDASKLNENVCRNPDGDAHGPW 420  
DB 387 YRNGNGNVMNLSQRTSSGLTCSMMDKNMMDLHRHIFWEPDASKLNENVCRNPDGDAHGPW 446  
QY 421 CYTGNPLIPMDYCPISRCEGDTPTIV 447  
DB 447 CYTGNPLIPMDYCPISRCEGDTPTIV 473

Search completed: October 3, 2005, 07:42:28  
Job time : 243.355 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:32 ; Search time 1375.69 Seconds  
(without alignments)  
24.255 Million cell updates/sec

Title: US-09-674-377B-1

Perfect score: 2604  
Sequence: 1 EKKRRNTIHEFKSAKTLTI.....IPWDYCPISRCBGDTPTTIV 447

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2601	99.9	697	2	US-08-460-890A-50 Sequence 50, Appl
2	2601	99.9	697	3	US-08-167-641C-50 Sequence 50, Appl
3	2601	99.9	697	3	US-08-460-971A-50 Sequence 50, Appl
4	2601	99.9	697	3	US-08-462-040-50 Sequence 50, Appl
5	2601	99.9	728	1	US-07-815-333A-2 Sequence 2, Appl
6	2601	99.9	728	4	US-08-087-783A-22 Sequence 22, Appl
7	2601	99.9	728	4	US-08-605-221-2 Sequence 2, Appl
8	2563.5	98.4	487	4	US-09-601-040A-27 Sequence 27, Appl
9	2563.5	98.4	717	4	US-09-601-040A-6 Sequence 8, Appl
10	2563.5	98.4	717	4	US-09-601-040A-8 Sequence 6, Appl
11	2563.5	98.4	723	1	US-07-838-410-1 Sequence 1, Appl
12	2563.5	98.4	723	1	US-08-290-937B-1 Sequence 1, Appl
13	2563.5	98.4	723	1	US-08-290-937B-2 Sequence 1, Appl
14	2563.5	98.4	723	1	US-08-404-643-1 Sequence 1, Appl
15	2563.5	98.4	723	1	US-09-194-326-1 Sequence 1, Appl
16	2563.5	98.4	723	4	US-09-600-991-18 Sequence 18, Appl
17	2563.5	98.4	723	4	US-08-605-221-4 Sequence 4, Appl
18	2563.5	98.4	723	4	US-09-601-040A-10 Sequence 10, Appl
19	2563.5	98.4	723	4	US-09-601-040A-2 Sequence 4, Appl
20	2563.5	98.4	729	4	US-09-601-040A-4 Sequence 4, Appl
21	2560.5	98.3	723	3	US-08-030-410-3 Sequence 3, Appl
22	2557.5	98.2	723	1	US-08-290-937B-3 Sequence 3, Appl
23	2541.5	97.6	723	3	US-09-194-326-2 Sequence 2, Appl
24	2541.5	97.6	723	3	US-08-700-519J-18 Sequence 18, Appl
25	2539.5	97.5	723	3	US-09-194-326-3 Sequence 3, Appl
26	2539.5	97.5	723	3	US-08-700-519J-19 Sequence 19, Appl
27	1780.5	68.4	574	4	US-09-600-991-2 Sequence 2, Appl

28	1471	56.5	290	4	US-08-484-841A-8 Sequence 8, Appl
29	1447.5	55.6	563	4	US-09-600-991-4 Sequence 4, Appl
30	1180.5	45.3	711	1	US-08-184-012C-8 Sequence 8, Appl
31	1180.5	45.3	711	1	US-08-334-177-2 Sequence 2, Appl
32	1180.5	45.3	711	2	US-08-666-082B-1 Sequence 1, Appl
33	1180.5	45.3	711	2	US-08-766-982-2 Sequence 2, Appl
34	1180.5	45.3	711	3	US-09-296-219-2 Sequence 2, Appl
35	1180.5	45.3	711	4	US-09-600-991-20 Sequence 20, Appl
36	1180.5	45.3	711	4	US-09-601-040A-12 Sequence 12, Appl
37	1180.5	45.3	711	4	US-09-949-016-6981 Sequence 6981, Ap
38	1180.5	45.3	711	5	PCT-US95-13830-2 Sequence 2, Appl
39	1125	43.2	716	2	US-08-766-982-1 Sequence 1, Appl
40	1125	43.2	716	3	US-09-296-219-1 Sequence 1, Appl
41	1066	40.9	790	4	US-08-991-761A-13 Sequence 13, Appl
42	1059	40.7	812	1	US-08-248-629A-1 Sequence 1, Appl
43	1059	40.7	812	1	US-08-451-932-1 Sequence 1, Appl
44	1059	40.7	812	1	US-08-452-260-1 Sequence 1, Appl
45	1059	40.7	812	1	US-08-326-785-1 Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-08-460-890A-50  
; Sequence 50, Application US/08460890A  
; Patent No. 5994109  
; GENERAL INFORMATION:  
; APPLICANT: Moo, Savio L.C.  
; APPLICANT: Smith, Louis C.  
; APPLICANT: Cristiano, Richard J.  
; APPLICANT: Gotchalk, Stephen  
; TITLE OR INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
; TITLE OR INVENTION: METHODS OF USE  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FASTSEQ for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,890A  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167,641  
; FILING DATE: December 14, 1993  
; APPLICATION NUMBER: 07/855,389  
; FILING DATE: March 20, 1992  
; APPLICATION NUMBER: PCT/US93/02725  
; FILING DATE: March 19, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; TELEPHONE/DOCKET NUMBER: 212/066  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 697 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-460-890A-50

Query Match 99.9%; Score 2601; DB 2; Length 697;  
Best Local Similarity 99.8%; Pred. No. 2.7e-214;  
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EKKRRNTIHEFKSAKTTLIKIDPALKIKYKVNADQCANRCTRNKGLPTCKAFVFDK 60
DB 1 QKRRNTIHEFKSAKTTLIKIDPALKIKYKVNADQCANRCTRNKGLPTCKAFVFDK 60
QY 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIGKRSYKGVSIITKSGIKOP 120
DB 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIGKRSYKGVSIITKSGIKOP 120
QY 121 WSSMTPIHHSFLPSSYRGKDLQENYCRNPRGEGGWCTSNPEVRYEVCIDIPQSEVYC 180
DB 121 WSSMTPIHHSFLPSSYRGKDLQENYCRNPRGEGGWCTSNPEVRYEVCIDIPQSEVYC 180
QY 181 MTCNGESYRGLMDHTESGKICQRMHDQTPHKKFLPERYPDKGFPDNNYCRNPDGQRPWC 240
DB 181 MTCNGESYRGLMDHTESGKICQRMHDQTPHKKFLPERYPDKGFPDNNYCRNPDGQRPWC 240
QY 241 YLDPHTRWECALIKTCADNTMNDTVDPLETTECIQGGEGYRGVNTIWMGIPQQRWDS 300
DB 241 YLDPHTRWECALIKTCADNTMNDTVDPLETTECIQGGEGYRGVNTIWMGIPQQRWDS 300
QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGDC 360
DB 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGDC 360
QY 361 YRGNKNYMGNIQSRTSGILTCGMDKXNMDLHRHIFWEPDASKLNENYCRNPDHAGPW 420
DB 361 YRGNKNYMGNIQSRTSGILTCGMDKXNMDLHRHIFWEPDASKLNENYCRNPDHAGPW 420
QY 421 CYTGNPLIPWDYCPISRCGDTTPTIV 447
DB 421 CYTGNPLIPWDYCPISRCGDTTPTIV 447

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## RESULT 2

US-08-167-641C-50  
Sequence 50, Application US/0816741C  
Patent No. 6033884

GENERAL INFORMATION:  
APPLICANT: MCO, Savio L. C.  
APPLICANT: Smith, Louis C.  
APPLICANT: Cristiano, Richard J.  
APPLICANT: Gottchalk, Stephen  
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
TITLE OF INVENTION: METHODS OF USE  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08167,641C  
FILING DATE: December 14, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/855,389

FILING DATE: March 20, 1992  
APPLICATION NUMBER: PCT/US93/02725  
FILING DATE: March 19, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 205/012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 697 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-167-641C-50

Query Match 99.9%; Score 2601; DB 3; Length 697;  
Best Local Similarity 99.8%; Pred. No. 2.7e-214;  
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EKKRRNTIHEFKSAKTTLIKIDPALKIKYKVNADQCANRCTRNKGLPTCKAFVFDK 60
DB 1 QKRRNTIHEFKSAKTTLIKIDPALKIKYKVNADQCANRCTRNKGLPTCKAFVFDK 60
QY 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIGKRSYKGVSIITKSGIKOP 120
DB 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIGKRSYKGVSIITKSGIKOP 120
QY 121 WSSMTPIHHSFLPSSYRGKDLQENYCRNPRGEGGWCTSNPEVRYEVCIDIPQSEVYC 180
DB 121 WSSMTPIHHSFLPSSYRGKDLQENYCRNPRGEGGWCTSNPEVRYEVCIDIPQSEVYC 180
QY 181 MTCNGESYRGLMDHTESGKICQRMHDQTPHKKFLPERYPDKGFPDNNYCRNPDGQRPWC 240
DB 181 MTCNGESYRGLMDHTESGKICQRMHDQTPHKKFLPERYPDKGFPDNNYCRNPDGQRPWC 240
QY 241 YLDPHTRWECALIKTCADNTMNDTVDPLETTECIQGGEGYRGVNTIWMGIPQQRWDS 300
DB 241 YLDPHTRWECALIKTCADNTMNDTVDPLETTECIQGGEGYRGVNTIWMGIPQQRWDS 300
QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGDC 360
DB 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGDC 360
QY 361 YRGNKNYMGNIQSRTSGILTCGMDKXNMDLHRHIFWEPDASKLNENYCRNPDHAGPW 420
DB 361 YRGNKNYMGNIQSRTSGILTCGMDKXNMDLHRHIFWEPDASKLNENYCRNPDHAGPW 420
QY 421 CYTGNPLIPWDYCPISRCGDTTPTIV 447
DB 421 CYTGNPLIPWDYCPISRCGDTTPTIV 447

```

## RESULT 3

US-08-460-971A-50  
Sequence 50, Application US/08460971A  
Patent No. 6150168

GENERAL INFORMATION:  
APPLICANT: MCO, Savio L. C.  
APPLICANT: Smith, Louis C.  
APPLICANT: Cristiano, Richard J.  
APPLICANT: Gottchalk, Stephen  
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
TITLE OF INVENTION: METHODS OF USE  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066



CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,971A  
FILING DATE: June 5, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/167,641  
FILING DATE: December 14, 1993  
APPLICATION NUMBER: 07/855,389  
FILING DATE: March 20, 1992  
APPLICATION NUMBER: PCT/US93/02725  
FILING DATE: March 19, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 212/063  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 697 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-460-971A-50

Query Match 99.9%; Score 2601; DB 3; Length 697;  
Best Local Similarity 99.8%; Pred. No. 2.7e-214;

Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRNTIHEPKSAKTTLIKIDPALKITKKVNTADOCANRTRNKGLPFTCKAFVFDK 60  
DB 1 ORKRNTIHEPKSAKTTLIKIDPALKITKKVNTADOCANRTRNKGLPFTCKAFVFDK 60  
QY 61 ARKQCLMPFPNMSGCVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKOP 120  
DB 61 ARKQCLMPFPNMSGCVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKOP 120  
QY 121 WSSMIPIHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCIDIPOCSEVBC 180  
DB 121 WSSMIPIHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCIDIPOCSEVBC 180  
QY 181 MTCNGESYRGKDLMDHTESGKICQRMHDQTPHRRKFLPERYPDKGFDNNYCRNPDGQPRWC 240  
DB 181 MTCNGESYRGKDLMDHTESGKICQRMHDQTPHRRKFLPERYPDKGFDNNYCRNPDGQPRWC 240  
QY 241 YTLDPHTTRWEYCAIKTCANNTMADTVPLETTECIGOGEGRGYNTITWNGIPQCRWMS 300  
DB 241 YTLDPHTTRWEYCAIKTCANNTMADTVPLETTECIGOGEGRGYNTITWNGIPQCRWMS 300  
QY 301 QYPIHEHDMTPENKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
DB 301 QYPIHEHDMTPENKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
QY 361 YRNGNGXNYMGNLSQTRSGILTCSMWDXMEDLHRIHFWEPDASKLNNENYCRNPDGDAHGM 420  
DB 361 YRNGNGXNYMGNLSQTRSGILTCSMWDXMEDLHRIHFWEPDASKLNNENYCRNPDGDAHGM 420  
QY 421 CYTGNPLIPWDYCPISRCGDTPTTV 447  
DB 421 CYTGNPLIPWDYCPISRCGDTPTTV 447

## RESULT 4

US-08-462-040-50  
Sequence 50, Application US/08462040  
Patent No. 617554

## GENERAL INFORMATION:

APPLICANT: Woo, Savio L.C.  
APPLICANT: Smith, Louis C.  
APPLICANT: Cristiano, Richard J.  
APPLICANT: Gottchalk, Stephen  
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
METHODS OF USE  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,040  
FILING DATE: June 5, 1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/167,641  
FILING DATE: December 14, 1993  
APPLICATION NUMBER: 07/855,389  
FILING DATE: March 20, 1992  
APPLICATION NUMBER: PCT/US93/02725  
FILING DATE: March 19, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 212/078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 697 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-462-040-50

Query Match 99.9%; Score 2601; DB 3; Length 697;  
Best Local Similarity 99.8%; Pred. No. 2.7e-214;

Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRNTIHEPKSAKTTLIKIDPALKITKKVNTADOCANRTRNKGLPFTCKAFVFDK 60  
DB 1 ERKRNTIHEPKSAKTTLIKIDPALKITKKVNTADOCANRTRNKGLPFTCKAFVFDK 60  
QY 61 ARKQCLMPFPNMSGCVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKOP 120  
DB 61 ARKQCLMPFPNMSGCVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKOP 120  
QY 121 WSSMIPIHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCIDIPOCSEVBC 180  
DB 121 WSSMIPIHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCIDIPOCSEVBC 180  
QY 181 MTCNGESYRGKDLMDHTESGKICQRMHDQTPHRRKFLPERYPDKGFDNNYCRNPDGQPRWC 240

DB 181 MTCNGESYRGLMDHTESGKICQRMWHOTPHRHKFLPERYPDKGPDNCRNPDGQPRPWC 240  
QY 241 YTLDPHTWEYCAIKTCADNTMNDTVDVPLETTECICQGGEGYRGVTWNTIMNGIPQGRWDS 300  
DB 241 YTLDPHTWEYCAIKTCADNTMNDTVDVPLETTECICQGGEGYRGVTWNTIMNGIPQGRWDS 300  
QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFITDPMIRVGYCSQIIPNCDSHGQDC 360  
DB 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFITDPMIRVGYCSQIIPNCDSHGQDC 360  
QY 361 YRGNGKNYMGNSQTRSGLTCSMDKXNMDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 420  
DB 361 YRGNGKNYMGNSQTRSGLTCSMDKXNMDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 420  
QY 421 CYTGNPLIPMDYCPISRCGDTTPTIV 447  
DB 421 CYTGNPLIPMDYCPISRCGDTTPTIV 447

## RESULT 5

US-07-815-333A-2  
Sequence 2, Application US/07815333A  
Patent No. 5342831

GENERAL INFORMATION:  
APPLICANT: Nakamura, Toshikazu  
APPLICANT: Matsumoto, Kunio  
TITLE OF INVENTION: EPITHELIOCYTE GROWTH ACCELERATOR  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Voit & Mayer  
STREET: Two Prudential Plaza, Suite 4900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/815.333A  
FILING DATE: 19911227  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Robert F.  
REGISTRATION NUMBER: 27555  
REFERENCE/DOCKET NUMBER: 44069  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 616-5600  
TELEFAX: (312) 616-5700  
TELEX: 25-3533  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 728 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-815-333A-2

Query Match 99.9%; Score 2601; DB 1; Length 728;  
Best Local Similarity 99.8%; Pred. No. 2.9e-214;  
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRNTHTEPKKSAKTTLIKIDPLAKITKKNVNTADQCANCTNNKGLPTCKAFVFDK 60  
DB :|||||  
QY 32 QKRNNTTHTEPKKSAKTTLIKIDPLAKITKKNVNTADQCANCTNNKGLPTCKAFVFDK 91  
DB :|||||  
QY 61 ARKQCLWFPNMSGGVKKEPFGEFDLVENKDYINNCIIIGKRSYKGTWSTIKSGIKOP 120  
DB :|||||  
QY 92 ARKQCLWFPNMSGGVKKEPFGEFDLVENKDYINNCIIIGKRSYKGTWSTIKSGIKOP 151  
DB :|||||

QY 121 WSMNIPHEHSFLBSSYRGKDLQENYCRNPRGEGGPMCFSTSNPEVRYEVCIDIPQCSVEEC 180  
DB 152 WSMNIPHEHSFLBSSYRGKDLQENYCRNPRGEGGPMCFSTSNPEVRYEVCIDIPQCSVEEC 211  
QY 181 MTCNGESYRGLMDHTESGKICQRMWHOTPHRHKFLPERYPDKGPDNCRNPDGQPRPWC 240  
DB 212 MTCNGESYRGLMDHTESGKICQRMWHOTPHRHKFLPERYPDKGPDNCRNPDGQPRPWC 271  
QY 241 YTLDPHTWEYCAIKTCADNTMNDTVDVPLETTECICQGGEGYRGVTWNTIMNGIPQGRWDS 300  
DB 272 YTLDPHTWEYCAIKTCADNTMNDTVDVPLETTECICQGGEGYRGVTWNTIMNGIPQGRWDS 331  
QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFITDPMIRVGYCSQIIPNCDSHGQDC 360  
DB 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFITDPMIRVGYCSQIIPNCDSHGQDC 391  
QY 361 YRGNGKNYMGNSQTRSGLTCSMDKXNMDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 420  
DB 392 YRGNGKNYMGNSQTRSGLTCSMDKXNMDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 451  
QY 421 CYTGNPLIPMDYCPISRCGDTTPTIV 447  
DB 452 CYTGNPLIPMDYCPISRCGDTTPTIV 478

## RESULT 6

US-08-087-783A-2  
Sequence 22, Application US/08087783A  
Patent No. 5547856

GENERAL INFORMATION:  
APPLICANT: Godowski, Paul J., Lokker, Nathalie A., Mark, Melanie R.  
TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR VARIANTS  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/087.783A  
FILING DATE: 13-Jul-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/884811  
FILING DATE: 18-MAY-92  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/885971  
FILING DATE: 18-MAY-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P0755779P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5416  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 728 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-087-783A-2

Query Match 99.9%; Score 2601; DB 1; Length 728;  
Best Local Similarity 99.8%; Pred. No. 2.9e-214;  
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ERKRRTIHEFKSAKTLIKIDPAKIKTKKVNATADOCANRCTRNGKLPFTCKAFVFDK 60
Db 32 QRRKRRTIHEFKSAKTLIKIDPAKIKTKKVNATADOCANRCTRNGKLPFTCKAFVFDK 91
QY 61 ARKQCLMFPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITSGIKCOP 120
Db 92 ARKQCLMFPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITSGIKCOP 151
QY 121 WSSMIPIHEHSFLPSSYRGKDLQENYCNPRGEGGPMCFSTSNPEVRYEVCIDIQCSEVFC 180
Db 152 WSSMIPIHEHSFLPSSYRGKDLQENYCNPRGEGGPMCFSTSNPEVRYEVCIDIQCSEVFC 211
QY 181 MTCNGESYRGKDLMDHTESGKICQRMWDHQPRIHKKFLPERYPDKGFDNNYCNPNPDGAPRPMC 240
Db 212 MTCNGESYRGKDLMDHTESGKICQRMWDHQPRIHKKFLPERYPDKGFDNNYCNPNPDGAPRPMC 271
QY 241 YTLDPHTRWYCAIKTCADNTMNDTVPLETTTECICOGGEGYRGVTNTIWNGIPCORWDS 300
Db 272 YTLDPHTRWYCAIKTCADNTMNDTVPLETTTECICOGGEGYRGVTNTIWNGIPCORWDS 331
QY 301 QYHEHDMTPENFKCDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGQDC 360
Db 332 QYHEHDMTPENFKCDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGQDC 391
QY 361 YRGNGKNYMGNLISQTSGLTCSMWDKNMEDLHRHIFWEPDASKLNNYCNPNPDGAPRPMC 420
Db 392 YRGNGKNYMGNLISQTSGLTCSMWDKNMEDLHRHIFWEPDASKLNNYCNPNPDGAPRPMC 451
QY 421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
Db 452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478
RESULT 7
US-08-605-221-2
; Sequence 2, Application US/08605221
; Patent No. 6699837
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Toshikazu
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE
; FILE REFERENCE: 2520-0101P
; CURRENT APPLICATION NUMBER: US/08/605,221
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: HGF-A (Full length HGF)
US-08-605-221-2
Query Match 99.9%; Score 2601; DB 4; Length 728;
Best Local Similarity 99.8%; Pred. No. 2,9e-214;
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ERKRRTIHEFKSAKTLIKIDPAKIKTKKVNATADOCANRCTRNGKLPFTCKAFVFDK 60
Db 32 QRRKRRTIHEFKSAKTLIKIDPAKIKTKKVNATADOCANRCTRNGKLPFTCKAFVFDK 91
QY 61 ARKQCLMFPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITSGIKCOP 120
Db 92 ARKQCLMFPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITSGIKCOP 151
QY 121 WSSMIPIHEHSFLPSSYRGKDLQENYCNPRGEGGPMCFSTSNPEVRYEVCIDIQCSEVFC 180
Db 152 WSSMIPIHEHSFLPSSYRGKDLQENYCNPRGEGGPMCFSTSNPEVRYEVCIDIQCSEVFC 211
QY 181 MTCNGESYRGKDLMDHTESGKICQRMWDHQPRIHKKFLPERYPDKGFDNNYCNPNPDGAPRPMC 240
Db 212 MTCNGESYRGKDLMDHTESGKICQRMWDHQPRIHKKFLPERYPDKGFDNNYCNPNPDGAPRPMC 271
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QY 241 YTLDPHTRWYCAIKTCADNTMNDTVPLETTTECICOGGEGYRGVTNTIWNGIPCORWDS 300
Db 272 YTLDPHTRWYCAIKTCADNTMNDTVPLETTTECICOGGEGYRGVTNTIWNGIPCORWDS 331
QY 301 QYHEHDMTPENFKCDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGQDC 360
Db 332 QYHEHDMTPENFKCDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGQDC 391
QY 361 YRGNGKNYMGNLISQTSGLTCSMWDKNMEDLHRHIFWEPDASKLNNYCNPNPDGAPRPMC 420
Db 392 YRGNGKNYMGNLISQTSGLTCSMWDKNMEDLHRHIFWEPDASKLNNYCNPNPDGAPRPMC 451
QY 421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
Db 452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478
RESULT 8
US-09-601-040A-27
; Sequence 27, Application US/09601040A
; Patent No. 6730657
; GENERAL INFORMATION:
; APPLICANT: MEDICO, Enzo et al.
; TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
; FILE REFERENCE: 0471-0161P
; CURRENT APPLICATION NUMBER: US/09/601,040A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-601-040A-27
Query Match 98.4%; Score 2563.5; DB 4; Length 487;
Best Local Similarity 98.7%; Pred. No. 2,8e-211;
Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;
QY 1 ERKRRTIHEFKSAKTLIKIDPAKIKTKKVNATADOCANRCTRNGKLPFTCKAFVFDK 60
Db 32 QRRKRRTIHEFKSAKTLIKIDPAKIKTKKVNATADOCANRCTRNGKLPFTCKAFVFDK 91
QY 61 ARKQCLMFPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITSGIKCOP 120
Db 92 ARKQCLMFPFNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITSGIKCOP 151
QY 121 WSSMIPIHEHSFLPSSYRGKDLQENYCNPRGEGGPMCFSTSNPEVRYEVCIDIQCSEVFC 180
Db 152 WSSMIPIHEH-----SYRGKDLQENYCNPRGEGGPMCFSTSNPEVRYEVCIDIQCSEVFC 206
QY 181 MTCNGESYRGKDLMDHTESGKICQRMWDHQPRIHKKFLPERYPDKGFDNNYCNPNPDGAPRPMC 240
Db 207 MTCNGESYRGKDLMDHTESGKICQRMWDHQPRIHKKFLPERYPDKGFDNNYCNPNPDGAPRPMC 266
QY 241 YTLDPHTRWYCAIKTCADNTMNDTVPLETTTECICOGGEGYRGVTNTIWNGIPCORWDS 300
Db 267 YTLDPHTRWYCAIKTCADNTMNDTVPLETTTECICOGGEGYRGVTNTIWNGIPCORWDS 326
QY 301 QYHEHDMTPENFKCDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGQDC 360
Db 327 QYHEHDMTPENFKCDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGQDC 386
QY 361 YRGNGKNYMGNLISQTSGLTCSMWDKNMEDLHRHIFWEPDASKLNNYCNPNPDGAPRPMC 420
Db 387 YRGNGKNYMGNLISQTSGLTCSMWDKNMEDLHRHIFWEPDASKLNNYCNPNPDGAPRPMC 446
QY 421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
Db 447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473
RESULT 9
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APPLICATION NUMBER: PCT/JP91/00942  
FILING DATE: 15-JUL-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 185852-1990  
FILING DATE: 13-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: WHITE, JOHN L.  
REGISTRATION NUMBER: 17,746  
REFERENCE/DOCKET NUMBER: WAK 110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
TELEX: 64191  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: Fibroblast  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 393..405 /note= "INTERNAL AMINO ACID  
OTHER INFORMATION: SEQUENCE IN ALPHA-CHAIN"  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 490..505 /note= "N-TERMINAL AMINO ACID  
OTHER INFORMATION: SEQUENCE OF BETA-CHAIN"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 605..623 /note= "INTERNAL AMINO ACID  
OTHER INFORMATION: SEQUENCE IN BETA-CHAIN"  
US-07-838-410-1

Query Match 98.4%; Score 2563.5; DB 1; Length 723;  
Best Local Similarity 98.7%; Pred. No. 4.7e-211;  
Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 EKKRRNTIEFKSAKTLTIKIDPALKIKTKKVNNTADQCANCTRNKKGLPFTCKAVFPK 60  
DB 32 QKRRNTIEFKSAKTLTIKIDPALKIKTKKVNNTADQCANCTRNKKGLPFTCKAVFPK 91  
QY 61 ARKQCLMPFPNMSGVKKFEGHEPDLYENKDIYINNCIIIGKRSYKGTVSITKSGIKCOP 120  
DB 92 ARKQCLMPFPNMSGVKKFEGHEPDLYENKDIYINNCIIIGKRSYKGTVSITKSGIKCOP 151  
QY 121 WSSMTPIHESFLPSSYRGKDLOENYCRNPRGEGGWCFTSNPEVRYEVCIDIPOCSEVEC 180  
DB 152 WSSMTPIHEH-----SYRGKDLOENYCRNPRGEGGWCFTSNPEVRYEVCIDIPOCSEVEC 206  
QY 181 MTCNGESYRGKLDHTHESGKICORWDHQTPIRHKFLPERYPDKGFDNRYCRNPDGGRPMC 240  
DB 207 MTCNGESYRGKLDHTHESGKICORWDHQTPIRHKFLPERYPDKGFDNRYCRNPDGGRPMC 266  
QY 241 YLLDPTHTWEYCAIKTCADNTMNDTVPLETTETCIQOGEGYRGVTNIIWNGIPQGRWDS 300  
DB 267 YLLDPTHTWEYCAIKTCADNTMNDTVPLETTETCIQOGEGYRGVTNIIWNGIPQGRWDS 326  
QY 301 QYRPHEDMTPEHFKCDLRENYCRNPDGSESPWCFTTDNIRYGSQIPNCMSHGQPC 360  
DB 327 QYRPHEDMTPEHFKCDLRENYCRNPDGSESPWCFTTDNIRYGSQIPNCMSHGQPC 386  
QY 361 YGNGKKNYGNLSQTRSGGLTCSWMDKNMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 420  
DB 387 YGNGKKNYGNLSQTRSGGLTCSWMDKNMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 446  
QY 421 CYTGNPLIPWDYCPISRCBGDTTPTIV 447

DB 447 CYTGNPLIPWDYCPISRCBGDTTPTIV 473

RESULT 12  
US-08-290-937B-1  
Sequence 1, Application US/08290937B  
Patent No. 5648233  
GENERAL INFORMATION:  
APPLICANT: YAMAGUCHI, KYOJI  
APPLICANT: SHIMA, NOBUYUKI  
APPLICANT: MURAKAMI, AKIHIKO  
APPLICANT: GOTO, MASAOKI  
APPLICANT: TSUDA, EISUKE  
APPLICANT: MASUNAGA, HIROAKI  
APPLICANT: TAKAHIRA, REIKO  
APPLICANT: OOGAKI, RUMIKO  
APPLICANT: UEDA, MASATSUGU  
APPLICANT: HIGASHIO, KANJI  
TITLE OF INVENTION: MODIFIED TCF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Testa, Hurwitz & Thibault  
STREET: 125 High St.  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,937B  
FILING DATE: 19-AUG-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, PAULA A.  
REGISTRATION NUMBER: 32,503  
REFERENCE/DOCKET NUMBER: FJN-022  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-290-937B-1

Query Match 98.4%; Score 2563.5; DB 1; Length 723;  
Best Local Similarity 98.7%; Pred. No. 4.7e-211;  
Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 EKKRRNTIEFKSAKTLTIKIDPALKIKTKKVNNTADQCANCTRNKKGLPFTCKAVFPK 60  
DB 32 QKRRNTIEFKSAKTLTIKIDPALKIKTKKVNNTADQCANCTRNKKGLPFTCKAVFPK 91  
QY 61 ARKQCLMPFPNMSGVKKFEGHEPDLYENKDIYINNCIIIGKRSYKGTVSITKSGIKCOP 120  
DB 92 ARKQCLMPFPNMSGVKKFEGHEPDLYENKDIYINNCIIIGKRSYKGTVSITKSGIKCOP 151  
QY 121 WSSMTPIHESFLPSSYRGKDLOENYCRNPRGEGGWCFTSNPEVRYEVCIDIPOCSEVEC 180  
DB 152 WSSMTPIHEH-----SYRGKDLOENYCRNPRGEGGWCFTSNPEVRYEVCIDIPOCSEVEC 206  
QY 181 MTCNGESYRGKLDHTHESGKICORWDHQTPIRHKFLPERYPDKGFDNRYCRNPDGGRPMC 240  
DB 207 MTCNGESYRGKLDHTHESGKICORWDHQTPIRHKFLPERYPDKGFDNRYCRNPDGGRPMC 266

QY 241 YTLDPHTRMEYCAIKTCADNTMNDTDVPLETTECIQOGGEGYRGTVNTIWMGIPCORWDS 300  
DB 267 YTLDPHTRMEYCAIKTCADNTMNDTDVPLETTECIQOGGEGYRGTVNTIWMGIPCORWDS 326  
QY 301 QYPHEHDMTPENFKCKDIRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
DB 327 QYPHEHDMTPENFKCKDIRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 386  
QY 361 YRGNGKNYMGNLSTQSRGLTCSMDKXNEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 420  
DB 387 YRGNGKNYMGNLSTQSRGLTCSMDKXNEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 446  
QY 421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447  
DB 447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473

RESULT 13  
US-08-290-937B-2  
; Sequence 2, Application US/08290937B  
; Patent No. 5648233  
; GENERAL INFORMATION:  
; APPLICANT: YAMAGUCHI, KYOJI  
; APPLICANT: SHIMA, NOBUYUKI  
; APPLICANT: MURAKAMI, AKIHIKO  
; APPLICANT: GOTO, MASAKI  
; APPLICANT: TSUDA, EISUKE  
; APPLICANT: MASUNAGA, HIROAKI  
; APPLICANT: TAKAHIRA, REIKO  
; APPLICANT: OOGAKI, FUMIKO  
; APPLICANT: UEDA, MASATSUGU  
; APPLICANT: HIGASHIO, KANUJI  
; TITLE OF INVENTION: MODIFIED TCF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Testa, Hurwitz & Thibault  
; STREET: 125 High St.  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/290,937B  
; FILING DATE: 19-AUG-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: FUN-022  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 723 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-290-937B-2

Query Match 98.4%; Score 2563.5; DB 1; Length 723;  
Best Local Similarity 98.7%; Pred. No. 4.7e-211;  
Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 EKKRRNTIEFKKSATYTIKIDPAKIKTKKYNVTDQCANCTRNKGLPFTCKAFVFDK 60  
DB 32 QKRRNTIEFKKSATYTIKIDPAKIKTKKYNVTDQCANCTRNKGLPFTCKAFVFDK 91

QY 61 ARKOLWFPEFMSGSYKKEFGHEFDLYENKDYIRNCIIGKRSYKGTVSITKSGIKOP 120  
DB 92 ARKOLWFPEFMSGSYKKEFGHEFDLYENKDYIRNCIIGKRSYKGTVSITKSGIKOP 151  
QY 121 WSMIPHEHSFLPSSYRKQDIQENYCRNPDGSESPWCFTTDPNIRVGYEVCIPCCSEYEC 180  
DB 152 WSMIPHEH-----SYGKDLQENYCRNPDGSESPWCFTTDPNIRVGYEVCIPCCSEYEC 206  
QY 181 MTCNGESYRGLMDHTESGKIQRWDPHHRKFLPERYPKGGPDNYCRNPDGPRWC 240  
DB 207 MTCNGESYRGLMDHTESGKIQRWDPHHRKFLPERYPKGGPDNYCRNPDGPRWC 266  
QY 241 YTLDPHTRMEYCAIKTCADNTMNDTDVPLETTECIQOGGEGYRGTVNTIWMGIPCORWDS 300  
DB 267 YTLDPHTRMEYCAIKTCADNTMNDTDVPLETTECIQOGGEGYRGTVNTIWMGIPCORWDS 326  
QY 301 QYPHEHDMTPENFKCKDIRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 360  
DB 327 QYPHEHDMTPENFKCKDIRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDC 386  
QY 361 YRGNGKNYMGNLSTQSRGLTCSMDKXNEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 420  
DB 387 YRGNGKNYMGNLSTQSRGLTCSMDKXNEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 446  
QY 421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447  
DB 447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473

RESULT 14  
US-08-404-643-1  
; Sequence 1, Application US/08404643  
; Patent No. 5658742  
; GENERAL INFORMATION:  
; APPLICANT: HIGASHIO, KANUJI  
; APPLICANT: SHIMA, NOBUYUKI  
; APPLICANT: OOGAKI, FUMIKO  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/404,643  
; FILING DATE: 15-MAR-1995  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: FUN-034 (3999/35)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 723 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-404-643-1

Query Match 98.4%; Score 2563.5; DB 1; Length 723;  
 Best Local Similarity 98.7%; Pred. No. 4.7e-211;  
 Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 EKKRRNTHEPKKSATTLIKIDPAKIKTKKVNVTADOCANRCTRNGKLPFTCKAFVPMK 60  
 :|||||  
 DB 32 QKRRNTHEPKKSATTLIKIDPAKIKTKKVNVTADOCANRCTRNGKLPFTCKAFVPMK 91  
 QY 61 ARKQCLMPFPNSMSGVKKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKCOP 120  
 :|||||  
 DB 92 ARKQCLMPFPNSMSGVKKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKCOP 151  
 QY 121 WSSMIPHEHSFLPSSYRGKDLOENYCRNPRGEGGWCFTSNPEVAYEVCIDIPOCSEVVC 180  
 :|||||  
 DB 152 WSSMIPHEH-----SYRGKDLOENYCRNPRGEGGWCFTSNPEVAYEVCIDIPOCSEVVC 206  
 QY 181 MTCNGESYRGKLDHDTESGKICORMDHOTPHRHKFLPERYPDKGFDNNYCRNPDGQRPWC 240  
 :|||||  
 DB 207 MTCNGESYRGKLDHDTESGKICORMDHOTPHRHKFLPERYPDKGFDNNYCRNPDGQRPWC 266  
 QY 241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIGOGEGYRGVTNTIINGIPCORWMS 300  
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 DB 267 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIGOGEGYRGVTNTIINGIPCORWMS 326  
 QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESFWCFTTDPNIRVGYCSQIPNCDSHGDQC 360  
 :|||||  
 DB 327 QYPHEHDMTPENFKCKDLRENYCRNPDGSESFWCFTTDPNIRVGYCSQIPNCDSHGDQC 386  
 QY 361 YRGNGKNYVGNLSQTRSGLTCSMDKMDLHRHIFWEPDASKLBNYCRNPDDAHGW 420  
 :|||||  
 DB 387 YRGNGKNYVGNLSQTRSGLTCSMDKMDLHRHIFWEPDASKLBNYCRNPDDAHGW 446  
 QY 421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447  
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 DB 447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473

RESULT 15  
 US-09-194-326-1  
 : Sequence 1, Application US/09194326  
 : Patent No. 6306827  
 : GENERAL INFORMATION:  
 : APPLICANT: Kinoseki, Masahiko  
 : APPLICANT: Ogawa, Hiroshi  
 : APPLICANT: Masanaga, Hiroaki  
 : APPLICANT: Kobayashi, Fumie  
 : APPLICANT: Yamaguchi, Kyoji  
 : APPLICANT: Higashio, Kanji  
 : TITLE OF INVENTION: Agent for Preventing and/or Treating Renal Disease  
 : FILE REFERENCE: FJN-069  
 : CURRENT APPLICATION NUMBER: US/09/194,326  
 : EARLIER FILING DATE: 1998-11-24  
 : EARLIER APPLICATION NUMBER: PCT/JP98/01221  
 : EARLIER FILING DATE: 1998-03-20  
 : EARLIER APPLICATION NUMBER: JP 94989  
 : NUMBER OF SEQ ID NOS: 3  
 : SOFTWARE: Patent Ver. 2.0  
 : SEQ ID NO 1  
 : LENGTH: 723  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 : FEATURE:  
 : OTHER INFORMATION: TCF-II  
 US-09-194-326-1

Query Match 98.4%; Score 2563.5; DB 3; Length 723;  
 Best Local Similarity 98.7%; Pred. No. 4.7e-211;  
 Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 EKKRRNTHEPKKSATTLIKIDPAKIKTKKVNVTADOCANRCTRNGKLPFTCKAFVPMK 60  
 :|||||  
 DB 32 QKRRNTHEPKKSATTLIKIDPAKIKTKKVNVTADOCANRCTRNGKLPFTCKAFVPMK 91

QY 61 ARKQCLMPFPNSMSGVKKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKCOP 120  
 :|||||  
 DB 92 ARKQCLMPFPNSMSGVKKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKCOP 151  
 QY 121 WSSMIPHEHSFLPSSYRGKDLOENYCRNPRGEGGWCFTSNPEVAYEVCIDIPOCSEVVC 180  
 :|||||  
 DB 152 WSSMIPHEH-----SYRGKDLOENYCRNPRGEGGWCFTSNPEVAYEVCIDIPOCSEVVC 206  
 QY 181 MTCNGESYRGKLDHDTESGKICORMDHOTPHRHKFLPERYPDKGFDNNYCRNPDGQRPWC 240  
 :|||||  
 DB 207 MTCNGESYRGKLDHDTESGKICORMDHOTPHRHKFLPERYPDKGFDNNYCRNPDGQRPWC 266  
 QY 241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIGOGEGYRGVTNTIINGIPCORWMS 300  
 :|||||  
 DB 267 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIGOGEGYRGVTNTIINGIPCORWMS 326  
 QY 301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESFWCFTTDPNIRVGYCSQIPNCDSHGDQC 360  
 :|||||  
 DB 327 QYPHEHDMTPENFKCKDLRENYCRNPDGSESFWCFTTDPNIRVGYCSQIPNCDSHGDQC 386  
 QY 361 YRGNGKNYVGNLSQTRSGLTCSMDKMDLHRHIFWEPDASKLBNYCRNPDDAHGW 420  
 :|||||  
 DB 387 YRGNGKNYVGNLSQTRSGLTCSMDKMDLHRHIFWEPDASKLBNYCRNPDDAHGW 446  
 QY 421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447  
 :|||||  
 DB 447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473

Search completed: October 3, 2005, 06:53:48  
 Job time : 1375.69 secs

**This Page Blank (uspto)**



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Copyright (c) 1993 - 2005 Comugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:29 ; Search time 39.775 Seconds  
(without alignments)  
1069.209 Million cell updates/sec

Title: US-09-674-377B-2

Perfect score: 2579  
Sequence: 1 EKRKRNTIHEFKSAKTLI.....IPWDYCPISRCGDTPTTV 442

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2563.5	99.4	728	1 JH0579	hepatocyte growth
2	2370.5	91.9	728	1 A60185	hepatocyte growth
3	2263.5	91.6	728	1 A35644	hepatocyte growth
4	1830	71.0	710	1 I51283	hepatocyte growth
5	1750	67.9	411	2 I51285	hepatocyte growth
6	1171	45.4	711	1 A47136	macrophage-stimula
7	1133.5	44.0	716	1 JCS061	macrophage-stimula
8	1114.5	43.2	716	1 A40332	macrophage-stimula
9	1054.5	40.9	790	1 PLPG	plasma (EC 3.4.21
10	1039.5	40.3	812	1 PLMS	plasma (EC 3.4.21
11	1036	40.2	810	2 I46260	plasma (EC 3.4.21
12	1021	39.6	810	2 B30848	plasma (EC 3.4.21
13	1019.5	39.5	812	2 B30848	plasma (EC 3.4.21
14	1018.5	39.5	810	1 PLBO	plasma (EC 3.4.21
15	927	35.9	2869	2 T1818	apolipoprotein(a)
16	864.5	33.5	4548	1 S00657	apolipoprotein(a) (EC
17	840	32.6	1420	2 A32869	apolipoprotein(a)
18	457	17.7	460	2 B61545	plasma (EC 3.4.21
19	450.5	17.5	455	2 A61545	plasma (EC 3.4.21
20	406	15.7	336	2 S33879	plasma precursor
21	357.5	13.9	625	1 TBBO	chrombin (EC 3.4.2
22	353	13.7	169	2 A40522	plasma (EC 3.4.21
23	352.5	13.6	618	2 A35827	chrombin (EC 3.4.2
24	350	13.3	612	1 TBHU	chrombin (EC 3.4.2
25	344	13.3	617	2 S10511	chrombin (EC 3.4.2
26	302.5	11.7	562	1 UKHUT	c-plasminogen acti
27	302	11.7	559	1 A35029	c-plasminogen acti
28	291	11.3	559	1 A29941	c-plasminogen acti
29	270	10.5	120	2 E61545	plasma (EC 3.4.21

30	268	10.4	123	2 C61545	plasma (EC 3.4.21
31	260.5	10.1	89	2 A60140	plasma (EC 3.4.21
32	237.5	9.2	946	1 A47299	ror-related recept
33	236.5	9.2	943	2 B45082	neurotrophic recep
34	228.5	8.9	603	2 S28941	coagulation factor
35	225	8.7	291	2 I38098	c-plasminogen acti
36	213.5	8.3	937	2 A45082	neurotrophic recep
37	204	7.9	655	1 A46688	hepatocyte growth
38	200	7.8	615	1 KFHU12	coagulation factor
39	192.5	7.5	558	2 JCS878	plasma hyaluronan-
40	189	7.3	593	2 S45281	coagulation factor
41	186.5	7.2	560	1 UC4795	plasma hyaluronan-
42	182.5	7.1	806	2 T18840	hypothetical prote
43	158.5	6.1	433	1 JN0560	u-plasminogen acti
44	158.5	6.1	685	1 A48289	neurotrophic recep
45	158	6.1	442	1 UKPG	u-plasminogen acti

## ALIGNMENTS

## RESULT 1

JH0579  
hepatocyte growth factor precursor [validated] - human  
N/Alternate names: hepatoleitin A, scatter factor  
C/Species: Homo sapiens (man)  
C/Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #ext change 09-Jul-2004  
C/Accession: JH0579; J00333; A41140; B36677; A33512; A39006; PH0114; A37796; S06  
R/Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.  
Gene 102, 213-219, 1991  
A/Title: Organization of the human hepatocyte growth factor-encoding gene.  
A/Reference number: JH0579; MUID:91340155; PMID:1831432  
A/Molecule type: DNA  
A/Residues: 1-728 <SEK>  
A/Cross-references: UNIPROT:P14210, DDBJ:D90318  
A/Note: The authors translated the codon GAA for residue 662 as Gly  
R/Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.  
Submitted to JIPID, March 1991  
A/Description: Organization of the human hepatocyte growth factor-encoding gene.  
A/Reference number: J00333  
A/Accession: J00333  
A/Molecule type: DNA  
A/Residues: 1-481, RT, 484-728 <SE2>  
R/Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H  
Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991  
A/Title: Evidence for the identity of human scatter factor and human hepatocyte growth f  
A/Reference number: A41140; MUID:9134393; PMID:1831266  
A/Accession: A41140  
A/Molecule type: mRNA  
A/Residues: 1-728 <WE1>  
A/Cross-references: GB:M72339; NID:9337935; PIDN:AAA64239.1; PID:9337936  
R/Seki, T.; Ihara, I.; Sugimura, A.; Shimomishi, M.; Nishizawa, T.; Asami, O.; Hagiya, i  
Biochem. Biophys. Res. Commun. 172, 321-327, 1990  
A/Title: Isolation and expression of cDNA for different forms of hepatocyte growth fact  
A/Reference number: A36677; MUID:91025062; PMID:2145836  
A/Accession: B36677  
A/Molecule type: mRNA  
A/Residues: 1-728 <SE3>  
A/Cross-references: GB:M60718; NID:9184031; PIDN:AAA52648.1; PID:9184032  
A/Accession: A36677  
A/Molecule type: mRNA  
A/Residues: 1-161, 167-728 <SE4>  
A/Cross-references: EMBL:X16323  
A/Experimental source: leukocyte  
R/Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakay  
Biochem. Res. Commun. 163, 967-973, 1989  
A/Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fac  
A/Reference number: A33512; MUID:89392017; PMID:2528952  
A/Accession: A33512  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-728 <M1>

A:Cross-references: GB:M29145; NID:9184044; PIDN:AAA52650.1; PID:9306846  
 R:Rubin, J.S.; Chan, A.M.L.; Botzaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hid  
 Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991  
 A:Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy  
 A:Reference number: A39006; MUID:91110540; PMID:1824873  
 A:Accession: A39006  
 A:Molecule type: mRNA  
 A:Residues: 1-161,167-728 <RUB>  
 A:Cross-references: GB:M55379  
 A:Experimental source: embryonic lung  
 R:Yoshiyama, Y.; Asakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama,  
 Biochem. Biophys. Res. Commun. 175, 660-667, 1991  
 A:Title: Identification of the N-terminal residue of the heavy chain of both native and  
 A:Reference number: PH0114; MUID:91207365; PMID:1826837  
 A:Accession: PH0114  
 A:Molecule type: protein  
 A:Residues: 32-43,53-58 <YOS>  
 A:Experimental source: plasma  
 R:Weidner, K.M.; Behrens, J.; Vandekekerckhove, J.; Birchmeier, W.  
 J. Cell Biol. 111, 2097-2108, 1990  
 A:Title: Scatter factor: molecular characteristics and effect on the invasiveness of epi  
 A:Reference number: A37796; MUID:91035621; PMID:2146276  
 A:Accession: A37796  
 A:Molecule type: protein  
 A:Residues: 86-91,329-344,356-363, 'XX', 366-370,425-434,442-447, 'X', 449-450,543-546, 'X', 5  
 R:Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimomishi, M.; Sugimura, A.; Tash  
 Nature 342, 440-443, 1989  
 A:Title: Molecular cloning and expression of human hepatocyte growth factor.  
 A:Reference number: S06794; MUID:90066676; PMID:2531289  
 A:Accession: S06794  
 A:Molecule type: mRNA  
 A:Residues: 1-31, 'KH', 34-77, 'N', 79-292, 'V', 294-299, 'M', 301-316, 'A', 318-335, 'K', 337-386, '  
 A:Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082  
 A:Experimental source: liver  
 A>Note: the authors translated the codon CAG for residue 727 as Glu  
 A>Note: part of this sequence, including the amino end of both the alpha and beta chains  
 R:Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchm  
 Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992  
 A:Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact  
 A:Reference number: I59214; MUID:93087571; PMID:1280830  
 A:Accession: I59214  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-288, 'ET', <HAR>  
 A:Cross-references: GB:I02931; NID:9184033; PIDN:AAA52649.1; PID:G184034  
 R:Miyaawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.  
 Eur. J. Biochem. 197, 15-22, 1991  
 A:Title: An alternatively processed mRNA generated from human hepatocyte growth factor g  
 A:Reference number: S15443; MUID:91200041; PMID:1826653  
 A:Accession: S15443  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-288, 'ET', <MIY2>  
 A:Cross-references: EMBL:X57574; NID:g32083; PIDN:CAA40802.1; PID:g32084  
 R:Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Muraikami, A.; Higashio, K.  
 Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991  
 A:Title: Tumor cytoxic factor/hepatocyte growth factor from human fibroblasts: cloning  
 A:Reference number: I52253; MUID:92062058; PMID:1835583  
 A:Accession: I52253  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 161-166 <SHI>  
 A:Cross-references: GB:S62561; NID:g237996; PIDN:AAB20169.1; PID:g237997  
 A:Accession: S62561  
 A:Molecule type: protein  
 A:Residues: 1-728 <SAS>  
 A:Cross-references: UNIPROT:O08048; GB:D10212; NID:g220435; PIDN:BA01064.1; PID:g220436  
 A:Experimental source: fibroblast, COS-1 cell  
 A>Note: submitted to JIPID, May 1993  
 A:Accession: PC2064  
 A:Molecule type: protein  
 A:Residues: 496-504 <SA2>  
 A:Note: does not have proteinase activity  
 C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1, kringle homolo

C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr  
 F:1-31/Domain: signal sequence #status predicted <SIG>  
 F:32-494,495-728/Product: hepatocyte growth factor #status experimental <MAT>  
 F:332-494/Domain: alpha chain #status experimental <ACH>  
 F:128-206/Domain: kringle homology <KR1>  
 F:211-288/Domain: kringle homology <KR2>  
 F:305-383/Domain: kringle homology <KR3>  
 F:391-469/Domain: kringle homology <KR4>  
 F:495-728/Domain: beta chain #status experimental <BCH>  
 F:495-716/Domain: trypsin homology <TRY>  
 F:332/Modified site: pyroglutamate carboxylic acid (Glu) (in mature form) #status experimen  
 F:294,402,566,653/Binding site: carbonyl site (Asn) (covalent) #status predicted  
 F:487-604/Disulfide bonds: #status predicted  
 Query Match 99.4%; Score 2563.5; DB 1; Length 728;  
 Best Local Similarity 98.7%; Pred. No. 1,66-175;  
 Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;  
 QY 1 ERKRNTIHEFKSAKTTLIKIDPALKIKTKVNTADQCANRCTRNKGLPFTCKAPVDPK 60  
 Db 32 QKRKRNTIHEFKSAKTTLIKIDPALKIKTKVNTADQCANRCTRNKGLPFTCKAPVDPK 91  
 QY 61 ARKQCLMPFNSMSGYKKEGHEFDLYENKDYRNCIGKRGYKTVSTTSGIKCP 120  
 Db 92 ARKQCLMPFNSMSGYKKEGHEFDLYENKDYRNCIGKRGYKTVSTTSGIKCP 151  
 QY 121 WSMIMPHHE-----SYRGKDLQENYCRNPRGEGGPMCFNSPEVREVCIDPQSEYEC 175  
 Db 152 WSMIMPHHEHSLPSYSYKCKDQENYCRNPREEGGPMCFNSPEVREVCIDPQSEYEC 211  
 QY 176 MTCNGESYRGIMDHTESGKICQRMWDHQTPIRHAKFLPERYPDKGFDDNYCRNPDQPPRWC 235  
 Db 212 MTCNGESYRGIMDHTESGKICQRMWDHQTPIRHAKFLPERYPDKGFDDNYCRNPDQPPRWC 271  
 QY 236 YTLDPHRTWEXCAIKTCADNTMNDTVDPIETETCIGOGSGSYRGTVMTINMGIPCOQPMDS 295  
 Db 272 YTLDPHRTWEXCAIKTCADNTMNDTVDPIETETCIGOGSGSYRGTVMTINMGIPCOQPMDS 331  
 QY 296 QYPRHDMTPNPFKCKDLRENYCRNPDGSESFWCTTDPNIRVGYCSQIPNCDMSHGQDC 355  
 Db 332 QYPRHDMTPNPFKCKDLRENYCRNPDGSESFWCTTDPNIRVGYCSQIPNCDMSHGQDC 391  
 QY 356 YRGNGKNYNGLSQTRSGILTSWMDKNMEDLHRII FNEPDASKLNENYCRNPDDDAHGPW 415  
 Db 392 YRGNGKNYNGLSQTRSGILTSWMDKNMEDLHRII FNEPDASKLNENYCRNPDDDAHGPW 451  
 QY 416 CYTGNPLIPMDYCPISRCESGDTTPTIV 442  
 Db 452 CYTGNPLIPMDYCPISRCESGDTTPTIV 478  
 RESULT 2  
 A60185  
 hepatocyte growth factor precursor - mouse  
 N:Alternate names: hepatocyte growth factor  
 C:Species: Mus musculus (house mouse)  
 C:Dates: 03-Mar-1993 #sequence revision 26-May-1994 #text change 09-Jul-2004  
 C:Accession: J02117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758; J00231  
 R:Saeki, M.; Nishio, M.; Saeki, T.; Enami, J  
 Biochem. Biophys. Res. Commun. 199, 772-779, 1994  
 A:Title: Identification of mouse mammary fibroblast-derived mammary growth factor as hep  
 A:Reference number: J02117; MUID:94183257; PMID:8135822  
 A:Accession: J02117  
 A:Molecule type: mRNA  
 A:Residues: 1-728 <SAS>  
 A:Cross-references: UNIPROT:O08048; GB:D10212; NID:g220435; PIDN:BA01064.1; PID:g220436  
 A:Experimental source: fibroblast, COS-1 cell  
 A>Note: submitted to JIPID, May 1993  
 A:Accession: PC2064  
 A:Molecule type: protein  
 A:Residues: 496-504 <SA2>  
 A:Note: does not have proteinase activity  
 R:Rosen, E.M.; Meisovsky, L.; Selter, E.; Vinter, D.W.; Goldberg, I.D.  
 Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990

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A>Title: Purified scatter factor stimulates epithelial and vascular endothelial cell mit
A:Reference number: A60185; MUID:90377927; PMID:2144630
A:Accession: A60185
A:Molecule type: protein
A:Residues: 'X',184-188,'KX',191-192,'X',194,'XX',197:357-364,'XX',367:375-377,'E',379,'
R.Liu, Y.; Michalopoulos, G.K.; Zarnegar, R.
Biochim. Biophys. Acta 1216, 299-303, 1993
A>Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth
A:Reference number: S43416; MUID:94060105; PMID:8241272
A:Accession: S43416
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-728 <LI>
A:Cross-references: EMBL.X72307
R.Liu, Y.
submitted to the EMBL Data Library, May 1993
A:Reference number: S45521
A:Accession: S45521
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-563,'H',565-728 <LI>
A:Cross-references: EMBL.X72307
R.Coffey, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.
Biochem. J. 278, 35-41, 1991
A>Title: Purification and characterization of biologically active scatter factor from rat
A:Reference number: S17173; MUID:91354223; PMID:1831975
A:Accession: S17173
A:Molecule type: protein
A:Residues: 496-517,'T',519 <Cof>
R.Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
A>Title: Hepatocytes and scatter factor.
A:Reference number: S10966; MUID:90326152; PMID:2142751
A:Accession: S10966
A>Status: preliminary
A:Molecule type: protein
A:Residues: 496-507,'X',509-512,'L',514-516,'X',518-519 <MAT>
R.Plascske-Schutter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.
J. Biol. Chem. 270, 830-836, 1995
A>Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
A:Reference number: I48758; MUID:95122532; PMID:7822318
A:Accession: I48758
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-30 <RES>
A:Cross-references: EMBL.X81630, MTD:9673451, PIDN:CA457286.1; PID:9673452
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C:Function:
A:Description: stimulates mitosis of hepatocytes and other cells
A>Note: does not have proteinase activity
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homold
C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; p
T:1-32/Domain: signal sequence #status predicted <SIG>
F:56-495/Domain: hepatocyte growth factor #status predicted <MAT>
F:56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F:129-207/Domain: kringle homology <KR1>
F:212-289/Domain: kringle homology <KR2>
F:306-384/Domain: kringle homology <KR3>
F:392-470/Domain: kringle homology <KR4>
F:496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F:496-719/Domain: trypsin homology <TRY>
F:33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature type) #status predicted
F:292,403,565/Binding site: carbonylde (Asn) (covalent) #status predicted
F:488-607/Disulfide bonds: #status predicted

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[illegible]

### RESULT 3

hepatocyte growth factor precursor - rat  
 NAlternate names: hepatopoietin A; scatter factor  
 CDate: 28-Sep-1990 #sequence\_revision 18-Nov-1992 #text\_change 09-Jul-2004  
 CAccession: A35644; S13211  
 R:Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimomishi, M.; Shimizu, S.; Nakamura, T.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990.  
 A>Title: Deduced primary structure of rat hepatocyte growth factor and expression of th  
 A:Reference number: A35644; MUID:90222197; PMID:2139229  
 A:Accession: A35644  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-728 <TMS>  
 A:Cross-references: UNIPROT:P17945; GB:D90102; GB:M32987; NID:g220766; PIDN:BA41133.1;  
 A:Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417  
 Eur. J. Biochem. 193, 375-381, 1990  
 R:Okajima, A.; Miyazawa, K.; Kitamura, N.  
 A>Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA du  
 A:Reference number: S13211; MUID:91031482; PMID:2146117  
 A:Accession: S13211  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-728 <OKA>  
 A:Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA8266.1; PID:g4539554  
 C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
 C:Function:  
 A:Description: stimulates mitosis of hepatocytes and other cells  
 A:Note: does not have proteinase activity  
 C:Keywords: hepatocyte growth factor/macrophage stimulating protein 1; kringle homol  
 C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; py  
 F:1-32/Domain: signal sequence #status predicted <SIG>  
 F:35-495/Product: hepatocyte growth factor #status predicted <MAT>  
 F:56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>  
 F:129-207/Domain: kringle homology <KR1>  
 F:212-289/Domain: kringle homology <KR2>  
 F:306-384/Domain: kringle homology <KR3>  
 F:393-470/Domain: kringle homology <KR4>  
 F:496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>  
 F:496-719/Domain: trypsin homology <TRY>  
 F:33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte  
 F:293,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:488-607/Disulfide bonds: #status predicted

Query Match 91.6%; Score 2363.5; DB 1; Length 728;  
Best Local Similarity 89.3%; Pred. No. 3.1e-161;  
Matches 399; Conservative 23; Mismatches 20; Indels 5; Gaps 1;

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QY 1 EKKRNTIHEFKKSAKTTLIKIDPALKITKKYVNTADOCANRCTRNGKLPTCKAFVFDK 60
DB 33 OKRRNTLHEFKKSAKTTLIKIDPALKITKKYVNTADOCANRCTRNGKLPTCKAFVFDK 92
QY 61 ARKOCMPFNSMSGVKKKFGHEPDLLENKDYIRNCIIIGKRSYKGTYSITKSGIKCOP 120
DB 93 SKRCKWYFNSMSGVKKKFGHEPDLLENKDYIRNCIIIGKRSYKGTYSITKSGIKCOP 152
QY 121 WSMI PHEH-----SYRGKLOENYCRNPRGEGGPMCTSNPEVRYEVCDIPOCSEVEC 175
DB 153 WMSMI PHEHSFLPSSYRGKLOENYCRNPRGEGGPMCTSNPEVRYEVCDIPOCSEVEC 212
QY 176 MTCNGESYRGKLDHDESGKICORMDHQTPIRHKFLPERYPDKGFDNNYCRNPDGQPRPWC 235
DB 213 MTCNGESYRGKLDHDESGKICORMDHQTPIRHKFLPERYPDKGFDNNYCRNPDGQPRPWC 272
QY 236 YTLDPHTREYCAIKTCADNTMNDTPVPLETTECIGOGEGYRGVTNTIWNGLPCORWDS 295
DB 273 YTLDPHTREYCAIKTCADNTMNDTPVPLETTECIGOGEGYRGVTNTIWNGLPCORWDS 332
QY 296 QYRPHEDMTPENFCKDLRENYCRNPDGSGSPMCTTDPNIRVGYCSQIPNCDSHGQDC 355
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DB 393 YGNGKNYKGNLSQTRSGITCSGMDKMDLHRHIFWEPDASKLBNYCRNPDGDAHGWC 452
QY 416 CYTGNDLIPMDYCPISRCGDTTPTIV 442
DB 453 CYTGNDLIPMDYCPISRCGDTTPTIV 479
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## RESULT 4

151283  
hepatocyte growth factor precursor - clawed frog  
N:Alternate names: heparinectin A; scatter factor  
C:Species: Xenopus sp. (clawed frog)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-May-2004  
C:Accession: I51283  
R:Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiohawa, K.  
Mech. Dev. 49, 123-131, 1995  
A:Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus ear  
A:Reference number: I51283; MUID:95267690; PMID:7748783  
A:Accession: I51283  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-710 <NAK>  
A:Cross-references: GB:S77422; NID:9998932; PIDN:AA834354.1; PID:9998933  
A>Note: the authors' translation for residue 458 (Thr) is inconsistent with the nucleoti  
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C:Function:  
A:Description: stimulates mitosis of hepatocytes and other cells  
A>Note: does not have proteinase activity  
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo  
C:Keywords: duplication; glycoprotein; growth factor; heterodimer; kringle  
F:42-477/478-709/Product: hepatocyte growth factor #status predicted <Mat>  
F:42-477/Domain: hepatocyte growth factor alpha chain #status predicted <Ach>  
F:115-193/Domain: kringle homology <KR1>  
F:198-275/Domain: kringle homology <KR2>  
F:289-367/Domain: kringle homology <KR3>  
F:375-453/Domain: kringle homology <KR4>  
F:478-709/Domain: hepatocyte growth factor beta chain #status predicted <BCh>  
F:52-128/Domain: trypsin homology <TRY>  
F:152-128, 281, 322, 379, 550, 637, 666/Binding site: carbohydrate (Aan) (covalent) #status pre  
F:470-588/Disulfide bonds: #status predicted

Query Match 71.0%; Score 1830; DB 1; Length 710;

Best Local Similarity 68.4%; Pred. No. 3.8e-123;  
Matches 301; Conservative 63; Mismatches 68; Indels 8; Gaps 2;

```
QY 3 KRRNTIHEFKKSAKTTLIKIDPALKITKKYVNTADOCANRCTRNGKLPTCKAFVFDK 62
DB 21 KRRNAPFDYKKTAEITLRLKALEVKTQNTTENCACKSRNGKLPFTCKAFAFDKI 80
QY 63 KQCLMPFNSMSGVKKKFGHEPDLLENKDYIRNCIIIGKRSYKGTYSITKSGIKCOPWS 122
DB 81 KRCHWFSFNTWSAGIKDYDISFDLYEKDYIRDCIIGKSGSNYGRNTVTKGLACQPMN 140
QY 123 SMIRPHEH-----YRGKLOENYCRNPRGEGGPMCTSNPEVRYEVCDIPOCSEVECMT 177
DB 141 SMIRPHEHFLPSTYRGKLOENYCRNPRGEGGPMCTSNPEVRYEVCDIPOCSEVECMT 200
QY 178 CNGESYRGKLDHDESGKICORMDHQTPIRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYT 237
DB 201 CNGEYRGPMDYTESGKCCORMDLORPHKHKFERERYPDKGLANNYCRNPDGQPRPWCYT 260
QY 238 LDPHTREYCAIKTCADNTMNDTPVPLETTECIGOGEGYRGVTNTIWNGLPCORWDSQY 297
DB 261 LDPHTREYCAIKTCADNTMNDTPVPLETTECIGOGEGYRGVTNTIWNGLPCORWDSQY 317
QY 298 PHEHDMTPENPKCKDLRENYCRNPDGSGSPMCTTDPNIRVGYCSQIPNCDSHGQDCYR 357
DB 318 PHLNHFTEENYKCKDLSENYCRNPDGSGSPMCTTDPNIRVGYCSQIPNCDSHGQDCYR 377
QY 358 GNGKNYKGNLSQTRSGITCSGMDKMDLHRHIFWEPDASKLBNYCRNPDGDAHGWCY 417
DB 378 GNGSYTKKTLRTFRPLPCSMWEKMDLKHHTREPVSLQKDYCRNPDGDAHGWCY 437
QY 418 TGNPLIPMDYCPISRCGDT 437
DB 438 TDDPFPMDYCPISRCGDT 457
```

## RESULT 5

151285  
hepatocyte growth factor/scatter factor - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I51285  
R:Steitl, A.; Stern, C.D.; They, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard  
Development 121, 813-824, 1995  
A:Title: A role for HGF/SF in neural induction and its expression in Hensen's node durin  
A:Reference number: I51285; MUID:95237013; PMID:7720585  
A:Accession: I51285  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-411 <STR>  
A:Cross-references: UNIPROT:Q90978; GB:S77480; NID:9998675; PID:9998676  
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo  
F:124-197/Domain: kringle homology <KR2>  
F:202-279/Domain: kringle homology <KR3>  
F:296-374/Domain: kringle homology <KR4>

Query Match 67.9%; Score 1750; DB 2; Length 411;  
Best Local Similarity 75.9%; Pred. No. 1.1e-117;  
Matches 289; Conservative 47; Mismatches 45; Indels 0; Gaps 0;

```
QY 3 KRRNTIHEFKKSAKTTLIKIDPALKITKKYVNTADOCANRCTRNGKLPTCKAFVFDKAR 62
DB 30 KRRNPLHDYKKTGELIMLIKVNKTLEVKTLNTEQCACRSRNKGLFTCKAFAVDRVT 89
QY 63 KQCLMPFNSMSGVKKKFGHEPDLLENKDYIRNCIIIGKRSYKGTYSITKSGIKCOPWS 122
DB 90 KRCHWLSNLSJLNGVRKKQDAFDFEKKDVRNCCIIGKGEYKGTISTISGICQAMN 149
QY 123 SMIRPHEH YRGKLOENYCRNPRGEGGPMCTSNPEVRYEVCDIPOCSEVECMT CNGES 182
DB 150 SMIRPHEH YRGKLOENYCRNPRGEGGPMCTSNPEVRYEVCDIPOCSEVECMT CNGES 209
QY 183 YRGLMDHDESGKICORMDHQTPIRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLDPHT 242
```

Db 210 YGPMPTHTSGKCEQCRWDLQRPKHKFRBERYPDKFDDNYCNRPDGKLRPMWCYTLDPT 269  
QY 243 RREYCAIKTCADNTMDTVPLETTECTICGGGSGYGVNTWNGIPCORMDSQYHEHD 302  
Db 270 PHEFCAIKTCIDVGLILSTENVAETTTICIGGGSGYGVNTWNGIQCCORMDSQYHEHD 329  
QY 303 MPENFKCDLRENNCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHQDCYRNGKN 362  
Db 330 ITPENFKCDLRENNCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHQDCYRNGKN 389  
QY 363 YMGNISQTRSGLTCSMWDKX 383  
Db 390 YMGNISQTRSGLTCSMWDKX 410

RESULT 6  
A:7136  
macrophage-stimulating protein 1 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 03-May-1994 #sequence revision 14-Nov-1997 #ext\_change 09-Jul-2004  
C:Accession: A40331; A40331; A47136; A61395  
R:Han, S.; Stuart, L.A.; Degen, S.J.F.  
Biochemistry 30, 9768-9780, 1991  
A:Title: Characterization of the DNFI52 locus on human chromosome 3: identification of  
A:Reference number: A40331; MUID:92002016; PMID:1655021  
A:Accession: A40331  
A:Molecule type: DNA  
A:Residues: 1-711 <HA1>  
A:Cross-references: UNIPROT:P26927; GB:M74179  
A:Accession: B40331  
A:Molecule type: mRNA  
A:Residues: 1-711 <HA2>  
A:Cross-references: GB:M74179; NID:g183976; PIDN:AA50165.1; PID:g183977  
R:Yoshimura, T.; Yuhki, N.; Wang, M.H.; Skeel, A.; Leonard, E.J.  
J. Biol. Chem. 268, 15461-15468, 1993  
A:Title: Cloning, sequencing, and expression of human macrophage stimulating protein (MS  
A:Reference number: A47136; MUID:93340141; PMID:8393443  
A:Accession: A47136  
A:Molecule type: mRNA  
A:Residues: 1-12, 'C', '14-622', 'F', '624-711' <YOS>  
A:Cross-references: GB:U1924; NID:g398037; PIDN:AA59872.1; PID:g398038  
A:Note: authors translated the codon TTT for residue 623 as Leu; parts of this sequence  
R:Skeel, A.; Yoshimura, T.; Showalter, S.D.; Tanaka, S.; Appella, E.; Leonard, E.J.  
J. Exp. Med. 173, 1227-1234, 1991  
A:Title: Macrophage stimulating protein: purification, partial amino acid sequence, and  
A:Reference number: A61395; MUID:91217635; PMID:1627141  
A:Accession: A61395  
A:Molecule type: protein  
A:Residues: 230-247,288-291, 'E', '293-295', 'X', '297-301', 'X', '303', 'E', '305', 'EX', '308-310,326-331  
A:Experimental source: plasma  
C:Genetics:  
A:Gene: GDB:MST1, D3P152, DNFI52, HGFL  
A:Cross-references: GDB:128833; OMIM:142408  
A:Map position: 3p21-3p21.3  
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringlike homolo  
C:Keywords: duplication; glycoprotein; growth factor; kringlike; plasma  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-483,484-711/Product: macrophage-stimulating protein 1 #status predicted <MA>  
F:19-483/Domain: alpha chain #status predicted <ACH>  
F:110-186/Domain: kringlike homology <KR1>  
F:191-268/Domain: kringlike homology <KR2>  
F:283-361/Domain: kringlike homology <KR3>  
F:370-448/Domain: kringlike homology <KR4>  
F:484-711/Domain: beta chain #status predicted <BCH>  
F:484-704/Domain: trypsin homology <TRY>  
F:56-78,60-66,110-166,131-169,157-181,191-268,212-251,240-263,283-361,304-343,332-355,37  
F:72,226,615/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 45.4%; Score 1171; DB 1; Length 711;  
Best Local Similarity 47.3%; Pred. No. 4,4e-76;  
Matches 196; Conservative 60; Mismatches 148; Indels 10; Gaps 4;

QY 33 VNTADQANRCCTRNKGLPPTCAKAFVDPKARKOCLWFPNMSGSGYKKEFGHEFDLYENKD 92  
Db 50 VADAECAARCC-----GPLLDCAAFHYNNVSSHCCQLLPWQHSLRAQDLHSSILCDLFOKDD 105  
QY 93 YTRNCTIGKRGYKGTSTITKSGIKCQPMSSMI PHEHSR---GKDLOENYCRNPGEGG 149  
Db 106 YVRTIMNNGVYRGTMATTVGGLPCQAMSHFPPDHKFTPTLRNGLEENFCRNPDGDFQ 165  
QY 150 GPMCFNSNEVYEVCDIPQCESEVCMTCNGESYRGLMDHTESGKICQRMHDQTPRRHKF 209  
Db 166 GPMCYTTDPAAVAFQSGCIGSCREAAACWNGSEYGAADRTSSGRBCQMWIDQHPHQEF 225  
QY 210 LPERYPDKGFDNNYCRNPDGQPRPWCYTLDPTTRWEYCAIKTCADNTMDTVPLETTEC 269  
Db 226 EPKFLDQGLDDNYCRNPDGSESPMCYTLDPTIERFCGLPRCGSEDAQROGA--TTVSC 283  
QY 270 ICGGSGYRGYNTWNGIPCORMDSQYHEHDMTPENFKCDLRENNCRNPDGSESPMC 329  
Db 284 FPKGEGYRGYNTWNGIPCORMDSQYHEHDMTPENFKCDLRENNCRNPDGSESPMC 343  
QY 330 FTTPNIRVGYCSQIPNC-DMSHGDCYRNGKNVWGNLSOTRSGLTCSMWDKXMDLHR 388  
Db 344 FTLRPEMRAFCYQIRCTDVPDPDCTHGAAGEQIRGYTSKTRKGVQCORMSAETPRHKQ 403  
QY 389 HIFWEPDASKLENYCRNPDGDAHGPMWCYTNPLIPWDYCPISRCGDTPTIV 442  
Db 404 FFTSEPHAQLEENFCRNPDGSHGPMWCYTMDPRPFDYCALRCADDQPSIL 457

RESULT 7  
JCS061  
macrophage-stimulating protein 1 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Jan-1997 #sequence revision 31-Jan-1997 #ext\_change 09-Jul-2004  
C:Accession: JCS061  
R:Yoshimura, K.; Iwano, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takasu, T.  
Biochem. Biophys. Res. Commun. 227, 273-280, 1996  
A:Title: Molecular cloning of rat macrophage-stimulating protein and its involvement in  
A:Reference number: JCS061; MUID:97011126; PMID:8858136  
A:Accession: JCS061  
A:Molecule type: mRNA  
A:Residues: 1-716 <ONS>  
A:Cross-references: P0521; EMBL:X95096; NID:g1669718; PIDN:CAA64473.1; PID:g166  
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringlike homolo  
C:Keywords: duplication; glycoprotein; growth factor; kringlike  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:32-488,489-716/Product: macrophage-stimulating protein 1 #status predicted <MA>  
F:32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>  
F:110-186/Domain: kringlike homology <KR1>  
F:191-268/Domain: kringlike homology <KR2>  
F:292-370/Domain: kringlike homology <KR3>  
F:379-457/Domain: kringlike homology <KR4>  
F:489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>  
F:489-709/Domain: trypsin homology <TRY>  
F:72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.0%; Score 1133.5; DB 1; Length 716;  
Best Local Similarity 46.1%; Pred. No. 2.1e-73;  
Matches 195; Conservative 68; Mismatches 141; Indels 19; Gaps 6;

QY 33 VNTADQANRCCTRNKGLPPTCAKAFVDPKARKOCLWFPNMSGSGYKKEFGHEFDLYENKD 92  
Db 50 VADAECAARCC-----GPLLDCAAFHYNNVSSHCCQLLPWQHSLRAQDLHSSILCDLFOKDD 105  
QY 93 YTRNCTIGKRGYKGTSTITKSGIKCQPMSSMI PHEHSR---GKDLOENYCRNPGEGG 149  
Db 106 YVRTIMNNGVYRGTMATTVGGLPCQAMSHFPPDHKFTPTLRNGLEENFCRNPDGDFQ 165  
QY 150 GPMCFNSNEVYEVCDIPQCESEVCMTCNGESYRGLMDHTESGKICQRMHDQTPRRHKF 209  
Db 166 GPMCYTTDPAAVAFQSGCIGSCREAAACWNGSEYGAADRTSSGRBCQMWIDQHPHQEF 225  
QY 210 LPERYPDKGFDNNYCRNPDGQPRPWCYTLDPTTRWEYCAIKTCADNTMDTVPLETTEC 269  
Db 226 EPKFLDQGLDDNYCRNPDGSESPMCYTLDPTIERFCGLPRCGSEDAQROGA--TTVSC 283  
QY 270 ICGGSGYRGYNTWNGIPCORMDSQYHEHDMTPENFKCDLRENNCRNPDGSESPMC 329  
Db 284 FPKGEGYRGYNTWNGIPCORMDSQYHEHDMTPENFKCDLRENNCRNPDGSESPMC 343  
QY 330 FTTPNIRVGYCSQIPNC-DMSHGDCYRNGKNVWGNLSOTRSGLTCSMWDKXMDLHR 388  
Db 344 FTLRPEMRAFCYQIRCTDVPDPDCTHGAAGEQIRGYTSKTRKGVQCORMSAETPRHKQ 403  
QY 389 HIFWEPDASKLENYCRNPDGDAHGPMWCYTNPLIPWDYCPISRCGDTPTIV 442  
Db 404 FFTSEPHAQLEENFCRNPDGSHGPMWCYTMDPRPFDYCALRCADDQPSIL 457

[illegible]

## RESULT 8

macrophage-stimulating protein 1 precursor - mouse  
N:Alternate names: hepatocyte growth factor- $\alpha$ -like protein  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C:Accession: A40332; B40332  
R:Degeen, S.-J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.  
Biochemistry 30, 9781-9791, 1991  
A:Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth factor  
A:Reference number: A40332; MUID:92002017; PMID:1832957  
A:Accession: A40332  
A:Molecule type: DNA  
A:Residues: 1-716 <DEG>  
A:CROSS-references: UNIPROT:P26528; GB:M74180; NID:G193831; PIDN:AAA50166.1; PID:G193833  
A:Accession: B40332  
A:Molecule type: mRNA  
A:Residues: 1-18, 'P', 20-716 <DEG2>  
A:CROSS-references: GB:M74181; NID:G193833; PIDN:AAA50167.1; PID:G193834  
C:Genetics:  
A:Introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 47  
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; Kringle homolo  
C:Keywords: duplication; glycoprotein; growth factor; Kringle  
F:1-11/Domain: signal sequence #status predicted <SIG>  
F:19-488, 489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>  
F:19-483/Domain: alpha chain #status experimental <ACH>  
F:110-186/Domain: Kringle homology <KR1>  
F:191-268/Domain: Kringle homology <KR2>  
F:292-370/Domain: Kringle homology <KR3>  
F:379-457/Domain: Kringle homology <KR4>  
F:488-711/Domain: beta chain #status experimental <BCH>  
F:489-709/Domain: tryptsin homology <TRY>  
F:72-173, 305, 620/Binding site: carboxydrate (Asn) (covalent) #status predicted  
F:72-173, 305, 620/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match Similarity	43.2%	Score 114.5	DB 1	Length 716
Best Local Similarity	45.9%	Pred. NO. 4.8e-72		
Matches 194; Conservative	67;	Mismatches 143;	Indels 19;	Gaps 6

[illegible][illegible]

## RESULT 9

Plasmin (EC 3.4.21.7) precursor - pig (fragment)  
N:Alternate names: plasminogen  
N:Contains: miniplasminogen  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 07-Sep-1990 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: S03733; S03737; A25834  
R:Schaller, J.; Marti, T.; Roesehaeet, S.J.; Kaempfer, U.; Rickli, E.E.  
A:Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca  
A:Reference number: S03733  
A:Accession: S03733  
A:Molecule type: protein  
A:Residues: 1-560 <SCH>  
A:Cross-references: UNIPROT:P06867  
R:Brunnholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Legier, W.; Manneberg, M.;  
Eur. J. Biochem. 114, 465-470, 1981  
A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,  
A:Reference number: S03735; MUID:91212097; PMID:7238497  
A:Accession: S03737  
A:Molecule type: protein  
A:Residues: 1-57 <BRU>  
R:Marti, T.; Schaller, J.; Rickli, E.E.  
Eur. J. Biochem. 149, 279-285, 1985  
A:Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.  
A:Reference number: A25834; MUID:85203907; PMID:3846553  
A:Accession: A25834  
A:Molecule type: protein  
A:Residues: 450-790 <MAR>  
A:Function:

A;Description: dissolves the walls of the grafts  
A;pathway: fibrinolysis

C;Superfamily plasmin; kringles  
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine protease

F.1-790/Product: plasminogen #status predicted <PRO>

F.1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLRH>

F.1-77/Domain: activation peptide #status predicted <APT>

F.78-560/Product: plasmin chain A #status predicted <ACH>

F.84-162/Domain: kringle homology <KR1>

F.166-243/Domain: kringle homology <KR2>

F.256-333/Domain: kringle homology <KR3>

F.358-435/Domain: kringle homology <KR4>

F.450-790/Product: miniplasminogen #status experimental <MIN>

F.461-540/Domain: kringle homology <KR5>

F.561-790/Product: plasmin chain B #status experimental <BCH>

F.561-783/Domain: trypsin homology <TRY>

F.30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305 bonds: #status predicted

i:602,645,740/Active site: His, Asp, Ser #status predicted



Query Match 40.9%; Score 1054.5; DB 1; Length 790;  
Best Local Similarity 44.6%; Pred. No. 1e-67;  
Matches 195; Conservative 64; Mismatches 133; Indels 45; Gaps 14;

25 ALKIKTKVNTADOCANRCCTRNKGLPFTCKAFVFDKARKOCOLMPFPMSSSGVKKERGH 84  
16 SLRKQVAASVEBCAKCAEETN--FICAFQYHSKDQCQVMAENSKTSPIARM--RD 71  
85 FDLVKNKYIRNCTIGKRSYKGTSTIKSGIKQPMSSMI PHEHSYRGK----DLQEN 139  
72 VVLFKRIYLSCEKGTGKNGYRGTTSTKSGVLCQKMSVSPH PKYSPEKPLAGLEEN 131  
140 YCANNPGEEGGPMCFNSPEVRYEVCIPQCEVECHTCNGESYRGLMDHTESGKICQRW 199  
132 YCANNPDDEKGPWCYTTPDPTRPDYCIPEC--EDECNHCSEHNEGKISKTMGIECQSW 190  
200 DHDTPHRHKFLPERYPKGFDDNYCRNPDGPRPWCYTLPDHRWEXCAIKTCADNTMD 259  
191 GSQSPHAGYLPKSPKPKMLKNNYCRNPDGPRPWCYTTPDKRWEFCDI-PRC--TTPP 248  
260 TDVPLETTECTIOGQEGYRGTVNTIWMGICQRMDSQYPHEHDMTPENFKCDLRENYCR 319  
249 TSGP--TYQCLKRGERYRTVSVTASGHTCQRMASQSPKHNRTPEPFCKLLENYCR 306  
320 NPDGSSPWCFTTDPNIRVGYCSQIPNCDS-----H-----GQDCYRGKN 362  
307 NPDGETAPWCYTTDSEVRMDYC--KIPSCGSTSTSTHLDAPVPEQTPVAQDCYRGNGS 365  
363 YMCNLQTSRGLCSMDKMDLHRIHFE-----PDASKLENYCRNPDGDAHGPWC 416  
366 YRSTSTTTTGRCQSVSMTP--HRH--EKTGPNFPNG-LTMNCRNPDAD-KSPWC 418  
417 YTGNPILPMDYCPISRC 433  
419 YTTDPVRWEXCNLKKC 435

Db

RESULT 10  
PLMS  
N:Contains: angiotensin; plasminogen  
C:Species: Mus musculus (house mouse)  
C>Date: 20-Sep-1991 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
C/Accession: A38514; S48202; S48203  
R/Begun, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.  
Genomics 8, 49-61, 1990  
A>Title: Characterization of the cDNA coding for mouse plasminogen and localization of  
A/Reference number: A38514; MUID:91184812; PMID:2081600  
A/Accession: A38514  
A:Molecule type: mRNA  
A:Residues: 1-812 <DEG>  
A/Cross-references: UNIPROT:P20918; GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g200403  
R/Lijfen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.  
Eur. J. Biochem. 224, 863-871, 1994  
A>Title: Characterization of the murine plasma fibrinolytic system.  
A/Reference number: S48202; MUID:95010076; PMID:7523120  
A/Accession: S48202  
A:Molecule type: protein  
A:Residues: 20-25 <LI>  
A/Accession: S48203  
A:Molecule type: protein  
A:Residues: 22-27 <LI>  
C/Comment: Plasminogen is synthesized by the kidney and is present in plasma and many of  
C/Comment: plasminogen is converted into plasmin by plasminogen activators, both plasmin  
C/Comment: immediately after dissociation from the clot. In the presence of the inhibitor, the activa  
C/Comment: e inhibitor, the activation involves also removal of the activation peptide.  
C/Comment: Stremelysin 1 (see PIR:KCMSI) acts on plasminogen to produce angiotensin. To  
C/Function: eful in treating solid tumors.  
A/Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va  
A/Pathway: fibrinolysis  
C:Superfamily: plasmin; kringie homology; plasminogen-related protein precursor homology

C/Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd  
F/1-96/Domain: plasminogen-related protein precursor homology <PLPH>  
F/1-19/Domain: signal sequence #status predicted <SIG>  
F/20-812/Product: plasminogen #status predicted <PRO>  
F/20-96/Domain: activation peptide #status predicted <APT>  
F/79-466/Product: angiotensin #status predicted <AST>  
F/97-581,582-812/Product: plasmin #status predicted <MAT>  
F/97-581/Domain: chain A #status predicted <ACH>  
F/103-181/Domain: kringie homology <KR1>  
F/185-262/Domain: kringie homology <KR2>  
F/275-352/Domain: kringie homology <KR3>  
F/377-454/Domain: kringie homology <KR4>  
F/461-560/Domain: kringie homology <KR5>  
F/582-812/Domain: chain B #status predicted <BCH>  
F/582-805/Domain: trypsin homology <TRY>  
F/49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,3  
bonds; #status predicted  
F/78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted  
F/136,308/Binding site: carboxylate (Asn) (covalent) #status predicted  
F/466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted  
F/581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental  
F/624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 40.3%; Score 1039.5; DB 1; Length 812;  
Best Local Similarity 43.1%; Pred. No. 1.2e-66;  
Matches 190; Conservative 64; Mismatches 144; Indels 43; Gaps 13;

30 TKKVNTA---DQANCTNKKGLPFTCKAFVFDKARKOCOLMPFPMSSSGVKKERGH 86  
37 TKQLAAGVSDCLACEBE--TDVCRSFQYHSKQOCQVMAENSKTSIIRM--RDVI 92  
87 LYENKDYIRNCTIGKRSYKGTSTIKSGIKQPMSSMI PHEHSYR-----GKDLQENY 141  
93 LPEKRYVLSCEKGTGKNGYRGTTSTKSGVLCQKMSVSPH PKYSPEKPLAGLEENY 152  
142 RNDPGEEGGPMCFNSPEVRYEVCIPQCEVECHTCNGESYRGLMDHTESGKICQRWD 201  
153 RNDNDGQGPWCYTTPDPTRPDYCIPEC--ECWYCSGEKYEKISKTMGIECQAMD 211  
202 QPFRHKFLPERYPKGFDDNYCRNPDGPRPWCYTLPDHRWEXCAIKTCADNTMD 261  
212 QSPHAGYLPKSPKPKMLKNNYCRNPDGPRPWCYTTPDKRWEFCDI-PRC--TTPP 267  
262 VPLETTECTIOGQEGYRGTVNTIWMGICQRMDSQYPHEHDMTPENFKCDLRENYCR 321  
268 PEPPTQCLKRGENYRTVSVTASGHTCQRMASQSPKHNRTPEPFCKLLENYCR 327  
322 DGSSEFWCFTTDPNIRVGYCSQIPNCDSHG-----ODCYRGKNY 364  
328 DGETAPWCYTTDSEVRMDYC--KIPSCSSASPDQSSVPEBQTPVQECYQSDQSYR 366  
365 GNLSQSRSLGTCSMMDKMDLHRIHFE---PDASKLENYCRNPDGDAHGPWCYTGNP 421  
387 GTSSTTTTGRCQSVSMTP--HRHKTPEPFDAK-LENNYCRNPDG-KGPWCYTTPD 442  
422 LIPMDYCPISRCGDTPTIV 442  
443 SVRMETCNLKR-SETGGSV 462

Db

RESULT 11  
146260  
N:Contains: angiotensin; plasminogen - western European hedgehog  
C/Species: Echinus europaeus (western European hedgehog)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
C/Accession: I46260  
R/Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fon  
J. Biol. Chem. 270, 24004-24009, 1995  
A>Title: The recurring evolution of Ipa(a): Insights from cloning of hedgehog apolipoprotei  
A/Reference number: I46259; MUID:96025778; PMID:7592597  
A/Accession: I46260  
A:Molecule type: mRNA  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-810 <LAW>  
 A:Cross-references: UNIPROT:029485; EMBL:U33171; NID:g1046360; PID:g1046361  
 C:Superfamily: plasmin: kringle homology; plasminogen-related protein precursor homology  
 C:Keywords: hydrolase; serine proteinase  
 F:103-181/Domain: plasminogen-related protein precursor homology <PLPH>  
 F:103-181/Domain: kringle homology <KR1>  
 F:185-262/Domain: kringle homology <KR2>  
 F:275-352/Domain: kringle homology <KR3>  
 F:379-456/Domain: kringle homology <KR4>  
 F:482-561/Domain: kringle homology <KR5>  
 F:582-803/Domain: trypsin homology <TRY>

Query Match 40.2%; Score 1036; DB 2; Length 810;  
 Best Local Similarity 43.8%; Pred. No. 2.2e-66;

Matches 192; Conservative 64; Mismatches 134; Indels 48; Gaps 14;

```

QY 30 TKK---VNTADQANRCIRNKGLPFTCKAFVFDKARKQCLMPFNSMSGYKKEGFED 86
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 37 TKKQLAGSTIECAKCEEE--EFTCRSFYHSKEQOCVMAENRKSIVFRM--RDV 92
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 LYENKDYIRNCIIIGKGRSYKGTVAITKSGIKQCPWSSMIPHEHSYR-----GKDLQENYC 141
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 93 LFEKMYLSECKVNGKNGKRYGTVAITKSGIKQCPWSSMIPHEHSYR-----GKDLQENYC 152
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 142 RNPGEBCGPMCFNSNPEVRYEVDIPQCEVECTNGESYRGLMDHTESGKICQAWDS 201
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 153 RNPDDPAGPMCFNSNPEVRYEVDIPQCEVECTNGESYRGLMDHTESGKICQAWDS 211
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 202 QTPRHKFLPERYPDKGFDNYCRNPDGQRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 261
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 212 QTPRHKFLPERYPDKGFDNYCRNPDGQRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 261
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 262 VPLE--TTECIQOGEGYRGTVAITWNGIPQCPWSSMIPHEHSYR-----GKDLQENYC 319
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 266 PPSGPTQCLKNGENRGDAVAVTSGTCHGMSAQTPHTHNTPEPFCKNDENYCR 325
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 330 NPDGSESPWCFCTTDPNIRVYCSQIPNCDMSH-----GDCYRANGK 362
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 336 NPDGSESPWCFCTTDPNIRVYCSQIPNCDMSH-----GDCYRANGK 362
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 361 KYMGNLSTRTSGGLTCSMDKXMDLHRIIFWE---PDASKLNEYCRNPDGAGP 417
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 QTYRGTSTTTTGKKCKQCPWTSMP--HRHSKTPENYDPAD--LTMYCNPAD--KGP 440
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 418 TGNPLIPMDYCPISRCEG 435
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 441 TTDPSEVRWEYCNLKKCSG 456
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

# RESULT 12

B30848  
 plasmin (EC 3.4.21.7) precursor - rhesus macaque  
 C:Species: Macaca mulatta (rhesus macaque)  
 C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
 C:Accession: B32869; B30848  
 R:Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.  
 J. Biol. Chem. 264, 5957-5965, 1989  
 A:Title: Rhesus monkey anolipoprotein(a). Sequence, evolution, and sites of synthesis.  
 A:Reference number: A32869; MUID:89174660; PMID:2825643  
 A:Accession: B32869  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-810 <TOM>  
 A:Cross-references: UNIPROT:P12545; GB:J04697; NID:g342272; PID:AAA6901.1; PID:g342272  
 C:Superfamily: Plasmin: kringle homology; plasminogen-related protein precursor homology  
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase  
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>  
 F:1-96/Domain: signal sequence #status predicted <SIG>  
 F:103-181/Domain: kringle homology <KR1>  
 F:185-262/Domain: kringle homology <KR2>  
 F:275-352/Domain: kringle homology <KR3>  
 F:379-456/Domain: kringle homology <KR4>  
 F:481-560/Domain: kringle homology <KR5>

F:581-803/Domain: trypsin homology <TRY>  
 F:49-73,53-61,103-181,124-154,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32  
 bonds: #status predicted  
 F:622,665,760/Active site: His, Asp, Ser #status predicted

Query Match 39.6%; Score 1021; DB 2; Length 810;  
 Best Local Similarity 42.2%; Pred. No. 2.6e-65;

Matches 186; Conservative 72; Mismatches 127; Indels 56; Gaps 13;

```

QY 30 TKK---VNTADQANRCIRNKGLPFTCKAFVFDKARKQCLMPFNSMSGYKKEGFED 86
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 37 TKKQLAGSTIECAKCEEE--EFTCRSFYHSKEQOCVMAENRKSIVFRM--RDV 92
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 LYENKDYIRNCIIIGKGRSYKGTVAITKSGIKQCPWSSMIPHEHSYR-----GKDLQENYC 141
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 93 LFEKMYLSECKVNGKNGKRYGTVAITKSGIKQCPWSSMIPHEHSYR-----GKDLQENYC 152
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 142 RNPGEBCGPMCFNSNPEVRYEVDIPQCEVECTNGESYRGLMDHTESGKICQAWDS 201
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 153 RNPDDPAGPMCFNSNPEVRYEVDIPQCEVECTNGESYRGLMDHTESGKICQAWDS 211
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 202 QTPRHKFLPERYPDKGFDNYCRNPDGQRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 261
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 212 QTPRHKFLPERYPDKGFDNYCRNPDGQRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 261
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 262 VPLE--TTECIQOGEGYRGTVAITWNGIPQCPWSSMIPHEHSYR-----GKDLQENYC 319
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 266 PPSGPTQCLKNGENRGDAVAVTSGTCHGMSAQTPHTHNTPEPFCKNDENYCR 325
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 330 NPDGSESPWCFCTTDPNIRVYCSQIPNCDMSH-----GDCYRANGK 362
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 336 NPDGSESPWCFCTTDPNIRVYCSQIPNCDMSH-----GDCYRANGK 362
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 361 KYMGNLSTRTSGGLTCSMDKXMDLHRIIFWE---PDASKLNEYCRNPDGAGP 414
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 YRGTSTTTTGKKCKQCPWTSMP--HRHSKTPENYDPAD--LTMYCNPAD--KGP 435
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 415 WCYTGNPLIPMDYCPISRCEG 435
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 436 WCYTGNPLIPMDYCPISRCEG 456
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

# RESULT 13

PLBO  
 plasmin (EC 3.4.21.7) precursor - bovine  
 N:Alternate names: plasminogen  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 30-Sep-1987 #sequence\_revision 28-Apr-1995 #text\_change 09-Jul-2004  
 C:Accession: S45046; A25835; I45961; S03736  
 R:Berghlund, L.; Andersen, M.D.; Petersen, T.E.  
 submitted to the EMBL Data Library, May 1994  
 A:Description: Cloning and characterization of the bovine plasminogen cDNA.  
 A:Reference number: S45046  
 A:Accession: S45046  
 A:Molecule type: mRNA  
 A:Residues: 1-812 <BER>  
 A:Cross-references: UNIPROT:P06868; EMBL:X79402; NID:g494962; PID:CAA55939.1; PID:g494949  
 A:Experimental source: liver  
 A>Note: it is uncertain whether Met-1 or Met-8 is the initiator  
 R:Schaller, J.; Moser, P.W.; Danneberg-Muller, G.A.K.; Roseliet, S.J.; Kamper, U.; Rick  
 Eur. J. Biochem. 149, 267-278, 1985  
 A:Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasmin  
 A:Reference number: A25835; MUID:85203906; PMID:3846532  
 A:Accession: A25835  
 A:Molecule type: protein  
 A:Residues: 27-334,'D',336-515,'H',517-554,'L',556-812 <SCH>  
 R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.  
 Biochemistry 23, 4243-4250, 1984  
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and  
 A:Accession: I45961  
 A:Status: translated from GB/EMBL/DBD  
 A:Molecule type: mRNA



A:Residues: 706-743,'R',745-812 <MAL>  
A:Cross-references: GB:K02935; NID:9163551; PIDN:AAA90714.1; PID:g163552  
R:Brumsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;  
Eur. J. Biochem. 114, 465-470, 1991  
A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,  
A:Reference number: S03735; MUID:81212097; PMID:7238497  
A:Accession: S03736  
A:Molecule type: protein  
A:Residues: 27-83 <BRU>  
C:Function:  
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va  
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act  
A:Pathway: fibrinolysis  
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology  
C:Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:8-103/Domain: plasminogen-related protein precursor homology <PLPH>  
F:27-812/Product: plasminogen #status experimental <PRO>  
F:27-103/Domain: activation peptide #status experimental <APR>  
F:104-583,584-812/Product: plasmin #status experimental <MAT>  
F:104-583/Domain: plasmin chain A #status experimental <ACH>  
F:110-188/Domain: plasmin chain A #status experimental <CR1>  
F:192-269/Domain: kringle homology <KR2>  
F:282-359/Domain: kringle homology <KR3>  
F:384-461/Domain: kringle homology <KR4>  
F:485-564/Domain: kringle homology <KR5>  
F:584-812/Domain: plasmin chain B #status experimental <BCH>  
F:584-805/Domain: trypsin homology <TRY>  
F:56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,33  
Donds: #status predicted  
F:315/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:365/Binding site: carbohydrate (Ser) (covalent) #status experimental  
F:624,667,762/Active site: His, Asp, Ser #status predicted  
Query Match 39.5%; Score 1019.5; DB 1; Length 812;  
Best Local Similarity 42.0%; Pred. No. 3,3e-85;  
Matches 183; Conservative 73; Mismatches 137; Indels 43; Gaps 12;  
25 ALKIKKVKNTADQCANRCRNKGLPFTCKAFVDFDARCKCLMFPPNSMSSGKKEFGHE 84  
42 SISRKKLGRSVEDCAKCC--EETTFVCFARFQYHSKEQCVMAENSKTVPFRM--RD 97  
85 FDLYENKDYIRNCLIGKGRSYKTVSITSGIKCQPMSSMIPIHESYRGK-----DLOEN 139  
98 VILYERKIRILLBEKTKNGQTYRGTETATETSGVTCQMSATSPHVPKFSPEKFLAELLEN 157  
140 YCRNPGEERGPGWCTSNPEVRYECDDIPQCSVEECMTONGESYRGLMDHTESGKICQRY 199  
158 YCRNPENDENGWPCYTTDDPKRYDCDIPEC--EDKCMHSGENYEKIKAKTMSGRDCQAW 216  
200 DHQTPHRRHFLPRRYDCKGDDNYCRNPGQGRPKWCYTLDPHTRWRYCAIKTCADNTMND 259  
217 DSQSPRAHGITPSKFPNKKLKNKYNCRNPGSEPRPKWCTTDPQKRWECDFPRT----- 270  
260 TDVPLE--TTECTIOGEGEYRGVTNTIANGIPICQRMDSQYPRHMDTPENFKCKDLRENY 317  
271 TPPSSGPKYQCLKGTGKQKYGVAVTESGHTCQRMSEQPRPHNNTPTENFPKULEENY 330  
318 CRNPDSSEPCWCTTDPNIRVYGCQIPIKNDMSH-----GODCYRGNG 360  
331 CRNPKECAKPCWCTTJNSEVREWEYCT--IPSCSSPLSTERMDVVPPEQTPVPDDCYHGNG 389  
361 KNYMGLSGOTRSLGTCQMDKXNEDJARRHFW--PDASKLNNYCRNPDADAHKPMKY 417  
390 QSYRGSTSTTITGRKQCSWSSMT--HRHUKTPENYPNAG--LTMNYCRNPDAD--KSPWCY 445  
418 TGNPLIPMDYCPISRC 433  
446 TTDPRVRWEFCNKKC 461

RESULT 14  
PLHU

plasmin (EC 3.4.21.7) precursor [validated] - human  
N:Alternate names: plasminogen precursor [misname]  
N:Containing: angiotensin; microplasmin; plasminogen  
C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence, revision 02-Dec-1994 #text, change 09-Jul-2004  
C:Accession: A35229; 152242; A26646; 162738; 184609; S03735; A00929; A04627; A04625; A0  
J. Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.  
R. Biol. Chem. 265, 6104-6111, 1990  
A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the fib  
A:Reference number: A35229; MUID:90202879; PMID:2318848  
A:Accession: A35229  
A:Molecule type: DNA  
A:Residues: 1-810 <DET>  
A:Cross-references: UNIPROT:P00747; UNIPROT:Q9UBQ9; UNIPROT:Q9UW12; GB:J05286; GB:M3427  
A:Experimental source: leukocyte; lung fibroblast  
R:Margaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; T  
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990  
A:Title: Definition of the transcription initiation site of human plasminogen gene in 1  
A:Reference number: 152242; MUID:91097523; PMID:2268308  
A:Accession: 152242  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-16 <MAL1>  
A:Cross-references: GB:M62890; NID:9190092; PIDN:AAA36454.1; PID:g553613  
R:Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.  
FEBS Lett. 213, 254-260, 1987  
A:Title: Molecular cloning and characterization of a full-length cDNA clone for human p  
A:Reference number: A26646; MUID:87162490; PMID:3030813  
A:Accession: A26646  
A:Molecule type: mRNA  
A:Residues: 1-471,'D',473-810 <FOR>  
A:Cross-references: GB:X05199; NID:935530; PIDN:CAA28831.1; PID:g35531  
A:Experimental source: liver  
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.  
Biochemistry 23, 4243-4250, 1984  
A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and  
A:Reference number: 145961; MUID:85023311; PMID:6148961  
A:Accession: 162738  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 292-471,'D',473-810 <MAL2>  
A:Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:g387031  
A:Accession: 184609  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 367-419 <MAL3>  
A:Cross-references: GB:K02921; NID:9190110; PIDN:AAA60123.1; PID:g190111  
R:Brumsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.  
Eur. J. Biochem. 114, 465-470, 1991  
A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,  
A:Reference number: S03735; MUID:81212097; PMID:7238497  
A:Accession: S03735  
A:Molecule type: protein  
A:Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOR>  
R:Brumsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.  
submitted to the Atlas, July 1997  
A:Reference number: A00929  
A:Accession: A00929  
A:Molecule type: protein  
A:Residues: 20-71,'E',73-76 <BRU>  
R:Brumsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.  
submitted to the Atlas, July 1997  
A:Reference number: A00929  
A:Accession: A00929  
A:Molecule type: protein  
A:Residues: 581-810 <W11>  
R:Wiman, B.; Wallen, P.  
Eur. J. Biochem. 50, 489-494, 1975  
A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human pl  
A:Reference number: A04625; MUID:75093329; PMID:122932  
A:Accession: A04625

A: Molecule type: protein  
A: Residues: 20-50,'Q','51-71','E','73-85,87-100 <M12>  
R: Wiman, B.; Wallen, P.  
Eur. J. Biochem. 58, 539-547, 1975  
A: Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen the  
A: Reference number: A04626; PMID:76043692; PMID:126863  
A: Accession: A04626  
A: Molecule type: Protein  
A: Residues: 483-507,'E',509-604 <M13>  
R: Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.  
J. Biol. Chem. 248, 1631-1633, 1973  
A: Title: The primary structure of human plasminogen. II. The histidine loop of human pla  
A: Reference number: A92125; PMID:73149248; PMID:4694729  
A: Contents: annotation; active site  
A: Groskopf, W.R.; Summaria, L.; Robbins, K.C.  
J. Biol. Chem. 244, 3590-3597, 1969  
A: Title: Studies on the active center of human plasmin. Partial amino acid sequence of a  
A: Reference number: A92048; PMID:69234739; PMID:4240117  
A: Contents: annotation; active site  
R: Texler, M.; Vail, Z.; Patchy, L.  
J. Biol. Chem. 257, 7401-7406, 1982  
A: Title: Structure of the omega-amino-carboxylic acid-binding sites of human plasminogen.  
A: Reference number: A93382; PMID:82213905; PMID:6919539  
A: Contents: annotation; omega-amino-carboxylic acid binding sites  
R: Vail, Z.; Patchy, L.  
J. Biol. Chem. 259, 13690-13694, 1984  
A: Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential  
A: Reference number: A92458; PMID:85054794; PMID:6094526  
A: Contents: annotation; fibrin binding site; omega-amino-carboxylic acid binding site  
R: Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soemmel, S.; McCance, S.G.;  
J. Biol. Chem. 271, 29461-29467, 1996  
A: Title: Kringe domains of human angiotensin. Characterization of the anti-proliferativ  
A: Reference number: A58811; PMID:97067211; PMID:8910613  
A: Contents: annotation  
R: Lijnen, H.R.; Uggv, F.; Bini, A.; Collen, D.  
Biochemistry 37, 4699-4702, 1998  
A: Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (M  
A: Reference number: A58812; PMID:9548733; PMID:9548733  
A: Contents: annotation  
R: Tulinsky, A.; Mulichak, A.M.  
Submitted to the Brookhaven Protein Data Bank, July 1991  
A: Reference number: A51341; PDB:1PK4  
A: Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454  
R: Tulinsky, A.; Wu, T.P.  
Submitted to the Brookhaven Protein Data Bank, July 1991  
A: Reference number: A51488; PDB:2PK4  
A: Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454  
R: Wu, T.P.; Tulinsky, A.  
Submitted to the Brookhaven Protein Data Bank, August 1993  
A: Reference number: A51911; PDB:1PKR  
A: Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181  
R: Padmanabhan, K.; Tulinsky, A.  
Submitted to the Brookhaven Protein Data Bank, April 1994  
A: Reference number: A52408; PDB:1PMK  
A: Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454  
R: Tulinsky, A.; Mathews, I.I.  
Submitted to the Brookhaven Protein Data Bank, December 1995  
A: Reference number: A65244; PDB:1CEA  
A: Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181  
R: Tulinsky, A.; Mathews, I.I.  
Submitted to the Brookhaven Protein Data Bank, December 1995  
A: Reference number: A65245; PDB:1CEB  
A: Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181  
R: Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.  
Biochemistry 30, 10576-10588, 1991  
A: Title: Crystal and molecular structure of human plasminogen kringe 4 refined at 1.9 Å  
A: Reference number: A58819; PMID:92031502; PMID:1657148  
A: Contents: annotation  
R: Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.  
Biochemistry 30, 10589-10594, 1991  
A: Title: The refined structure of the epsilon-amino-carboxylic acid complex of human plasmin  
A: Reference number: A58818; PMID:92031503; PMID:1657149  
A: Contents: annotation

R: de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.  
Biochemistry 31, 270-279, 1992  
A: Title: Crystal structure of the kringe 2 domain of tissue plasminogen activator at 2.  
A: Reference number: A39483; PMID:9218803; PMID:1310033  
A: Contents: annotation; X-ray crystallography, 2.4 angstroms  
R: Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.  
Submitted to the Brookhaven Protein Data Bank, June 1995  
A: Reference number: A65980; PDB:1KRN  
A: Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454  
R: Rejzante, M.; Llinas, M.  
Submitted to the Brookhaven Protein Data Bank, August 1996  
A: Reference number: A65803; PDB:1HPJ  
A: Contents: annotation; conformation by (1)H-NMR, residues 103-181  
R: Rejzante, M.; Llinas, M.  
Submitted to the Brookhaven Protein Data Bank, August 1996  
A: Reference number: A65804; PDB:1HPK  
A: Contents: annotation; conformation by (1)H-NMR, residues 103-181  
R: Rejzante, M.R.; Llinas, M.  
Eur. J. Biochem. 221, 927-937, 1994  
A: Title: (1)H-NMR assignments and secondary structure of human plasminogen kringe 1.  
A: Reference number: A43645; PMID:94237157; PMID:8181475  
A: Contents: annotation; conformation by (1)H-NMR, residues 96-184  
R: Rejzante, M.R.; Llinas, M.  
Eur. J. Biochem. 221, 939-949, 1994  
A: Title: Solution structure of the epsilon-amino-hexanoic acid complex of human plasminog  
A: Reference number: A58817; PMID:94237158; PMID:8181476  
A: Contents: annotation; conformation by (1)H-NMR  
C: Comment: plasminogen is synthesized by the kidney and is present in plasma and many ot  
C: Comment: plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU a  
d PIR:FGU8B).  
C: Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITNUA2) immediately af  
ter-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor,  
C: Comment: Microplasmin is formed by autocytic cleavage of plasmin under artificial cond  
C: Comment: Stromelysin 1 (see PIR:KCHU51) acts on plasminogen to produce angiotensin. Tc  
ting solid tumors.  
C: Genes: GDB:PLG  
A: Gene: GDB:PLG  
A: Cross-references: GDB:119498; OMIM:173350  
A: Map position: 6q26-6q27  
A: Intons: 17/1, 62/2, 98/1, 136/2, 183/1, 223/2, 263/1, 317/2, 366/1, 419/2, 480/1, 529  
C: Function:  
A: Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va  
nab the walls of the graafian follicle; also activates the urokinase-type plasminogen act  
A: Pathway: fibrinolysis  
C: Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology  
C: Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr  
F:1-19/Domain: plasminogen-related protein precursor homology <PLBP>  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-810/Product: plasminogen #status experimental <PRO>  
F:20-96/Domain: activation peptide #status experimental <AP>  
F:79-466/Product: angiotensin #status experimental <AST>  
F:97-580, 581-810/Product: plasmin #status experimental <MAT>  
F:97-580/Domain: plasmin chain A #status experimental <CHA>  
F:103-181/Domain: kringe homology <KR1>  
F:185-262/Domain: kringe homology <KR2>  
F:275-352/Domain: kringe homology <KR3>  
F:377-454/Domain: kringe homology <KR4>  
F:481-560/Domain: kringe homology <KR5>  
F:550-580, 581-810/Product: microplasmin #status experimental <MMT>  
  
Query Match 39.5%; Score 1018.5; DB 1; Length 810;  
Best local Similarity 43.1%; Pred. No. 3.9e-65;  
Matches 191; Conservative 67; Mismatches 138; Indels 47; Gaps 14;  
  
QY 30 TKK---VMTADCARCTRNKGLPPTCAFAVEDKARKKQCLMPPNMSGGVKKEGHEPD 86  
DB 37 TKKQAGSIEBCAKKCEBDE--EFTCFAPQVHSKQOCQVIAENRKSIIIRM--RDVV 92  
QY 87 LYENKDYIRNCTIGKGRSYKGTSTKSGIKCOQPMSPHRE----HSYRGKDLOENYC 141  
DB 93 LEKVKYVLSSECKTGNGKVKYRGTMSTKTKGKITQCKMSSTPHRPRSPAHHPBEGLEENYC 152  
QY 142 RNPREGGPGWCFTSNPEVRYEVCIDIPOCSVEVCMTNGESYRGLMDHTESGKICORMDH 201

Db 153 RNPENDPQGPWCYTTDPERKYDCDILECEE-ECMHCSGNNYDGKISKTMSSGLECQAMDS 211  
QY 202 QTPHRKFTLPERYPDGDNDNYCRNPDGQRPWCYTLDPHTREYCAIKTCADNTMNDND 261  
Db 212 QSPHAGYIPSKPKPKNLKKNYCRNPDRELPRPCFTTDPKRELCDIPRCT-----TP 265  
QY 262 VPLE--TTECIOGQGGYRGVTNTIWNGLPCQWRMSQYPHEHDMTPENFKCDLRENYCR 319  
Db 266 PSSSGFTYQCLKGTGENYGNVAVTVSGHTCQWMSAQTPHTNRTPENFPCKNLDENYCR 325  
QY 320 NPDGSESPWCFTTDPPIRIGYCSQIPNCDSH-----GQDCYRGNGKN 362  
Db 326 NPDGKAPWCHTNSQVRWEYC-KIPSCDSSPVSTEQLAPTAPPELTPVQDCYHGDGQS 384  
QY 363 YMGNLQSTRSGLTCSMMDKNMEDLHRHIFWE---PDASKLENYCRNPDGDAHGPWCYTG 419  
Db 385 YRGTSSTTTTGKKCCQMSMTF--HRHOKTPENYPNAG-LTMNYCRNPDAD-KGPWCFTT 440  
QY 420 NPLIPMDYCPISRCEGDTTPTIV 442  
Db 441 DPSVRWEYCNLKKCSG-TEASV 462

RESULT 15  
T18518  
apolipoprotein(a) - western European hedgehog (fragment)  
C:Species: Erinaceus europaeus (western European hedgehog)  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18518  
R:Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong  
J. Biol. Chem. 270, 24004-24009, 1995  
A>Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot  
A:Reference number: I46259; MIMD:96025778; PMID:7592597  
A:Accession: T18518  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2869 <LAI>  
A:Cross-references: UNIPROT:Q28398; EMBL:U31170; NID:g1046358; PID:g1046359; PIDN:AAC485  
A:Experimental source: liver  
C:Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, con  
ent apolipoprotein(a).

Query Match 35.9%; Score 927; DB 2; Length 2869;  
Best Local Similarity 45.4%; Pred. No. 4.9e-58;  
Matches 172; Conservative 50; Mismatches 123; Indels 34; Gaps 11;  
QY 89 ENKDYTRNCIIIGKRSYKGTVSITKSGIKQWSSMIPIEHS-----YRGKDLQENYCRN 143  
Db 2490 EPLDLVDQCLEGTGENYRGMAVTASGHTCQWRREQSPHSHSRTPENYPTKNLVGNYCRN 2549  
QY 144 PRGEBGSPWCFTSNPREVREVCIPQCSF-----VEGMCNGESYRGIMDHTS 192  
Db 2550 PDGEV-APWCYTTNSAMRWEYCSIPACESPTPTPEHLVVEQCLENGENYQGNMAITVS 2608  
QY 193 GKICQRMWDQTPHRHKLPERYPDKGFDNDNYCRNPDGQRPWCYTLDPHTREYCAIKTC 252  
Db 2609 GQPCQGMKQTPHRHKLPERYPDKGFDNDNYCRNPDGQRPWCYTLDPHTREYCAIKTC 2668  
QY 253 ADNTMNDTVPLETTCEIOGQGGYRGVTNTIWNGLPCQWRMSQYPHEHDMTPENFKCD 312  
Db 2669 -ESSSPTEPMIIPDQCLEGTGENYRGMAVTASGHTCQWRREQSPHSHSRTPENYPTKN 2727  
QY 313 LRENYCRNPDGSESPWCFTTDPPIRIGYCSQIPNCDSH-----GQDCYRGNGKN 364  
Db 2728 LRENYCRNPDGSESPWCFTTDPPIRIGYCSQIPNCDSH-----GQDCYRGNGKN 364  
QY 365 GNLQSTRSGLTCSMMDKNMEDLHRHIFWEBD--ASKLKNYCRNPDGDAHGPWCYTG 421  
Db 2787 GNLQSTRSGLTCSMMDKNMEDLHRHIFWEBD--ASKLKNYCRNPDGDAHGPWCYTG 421  
QY 422 LIPMDYCPISRCEGDTTPT 440

Db 2843 AVRWEYCSIPTCESPTPT 2861  
Search completed: October 3, 2005, 05:59:59  
Job time : 39.775 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:29 ; Search time 64.6344 Seconds  
(without alignments)  
3501.834 Million cell updates/sec

Title: US-09-674-377B-2

Perfect score: 2579  
Sequence: 1 EKRKNITHEFKSAKTLLI.....IPDYCPISRCBGGDTPTIV 442

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2563.5	99.4	728	1	HGF_HUMAN	P14210 homo sapien
2	2424.5	94.0	730	2	Q867B7	Q867B7 canis fam1
3	2418.5	93.8	730	2	Q76BS1	Q76BS1 bos taurus
4	2414.5	93.6	728	2	Q9HH09	Q9HH09 felis silve
5	2371.5	92.0	728	2	Q8C9G5	Q8C9G5 mus musculu
6	2370.5	91.9	728	1	HGF_MOUSE	Q08048 mus musculu
7	2363.5	91.6	728	1	HGF_RAT	P17945 rattus norv
8	2014.5	78.1	726	2	Q90978	Q90978 gallus gall
9	1830	71.0	710	2	Q91402	Q91402 xenopus. he
10	1718	66.6	405	2	Q788Q2	Q788Q2 gallus gall
11	1204.5	46.7	449	2	Q6GP14	Q6GP14 xenopus lae
12	1198.5	45.9	716	2	Q91691	Q91691 xenopus lae
13	1184	45.4	704	2	Q90865	Q90865 gallus gall
14	1171	45.4	711	1	HGFL_HUMAN	P26927 homo sapien
15	1163.5	45.1	717	2	P70006	P70006 mus musculu
16	1156	44.8	709	2	Q7ZTN9	Q7ZTN9 xenopus lae
17	1152.5	44.7	709	2	Q90ZNE	Q90ZNE brachydantio
18	1151	44.6	567	2	Q13708	Q13708 homo sapien
19	1133.5	44.0	716	2	P70521	P70521 rattus norv
20	1114.5	43.2	716	2	HGFL_MOUSE	P26928 mus musculu
21	1114.5	43.2	716	2	Q91XG8	Q91XG8 mus musculu
22	1073.5	41.6	818	2	Q6PBA6	Q6PBA6 brachydantio
23	1066	41.3	812	1	PLMN_RAT	001177 rattus norv
24	1066	40.9	806	1	PLMN_MACCU	018783 macropus eu
25	1054.5	40.5	790	1	PLMN_PIG	P06867 sus scrofa
26	1044.5	40.5	466	2	Q6TC10	Q6TC10 mus musculu
27	1044.5	40.3	812	1	PLMN_MOUSE	P20918 mus musculu
28	1040	40.3	215	2	O42341	O42341 gallus gall
29	1036	40.2	810	1	PLMN_BRIEU	Q29485 erinaceus e
30	1021	39.6	810	1	PLMN_MACMU	P12545 macaca mula
31	1019.5	39.5	812	1	PLMN_BOVIN	P06868 bos taurus

32	1018.5	39.5	810	1	PLMN_HUMAN	P00747 homo sapien
33	1013	39.3	759	2	Q7TP84	Q7TP84 rattus norv
34	971.5	37.7	359	2	Q8WMR1	Q8WMR1 canis fam1
35	958	37.1	648	2	Q9H1V4	Q9H1V4 homo sapien
36	927	35.9	2869	2	Q28398	Q28398 erinaceus e
37	864.5	33.5	4548	1	AP0A_HUMAN	P08519 homo sapien
38	858.5	33.3	211	2	Q55027	Q55027 mus musculu
39	840	32.6	1420	1	AP0A_MACMU	P14417 macaca mula
40	617	23.9	162	2	Q8C4E2	Q8C4E2 mus musculu
41	577.5	22.4	109	2	Q9N1B8	Q9N1B8 ovis aries
42	444.5	17.2	454	2	Q46506	Q46506 papio hamad
43	439	17.0	75	2	Q9BGN9	Q9BGN9 bos taurus
44	406	15.7	325	1	PLMN_PETMA	P33574 petromyzon
45	400	15.5	429	2	Q8AVB0	Q8AVB0 brachydantio

## ALIGNMENTS

```
RESULT 1
HGF_HUMAN                                PRT: 728 AA.
ID   P14210; Q02935; Q13494; Q14519; Q8TCE2; Q9BYU9; Q9BYMO; Q9UDU6;
AC   01-JAN-1990 (Rel. 13, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Hepatocyte growth factor precursor (Scatter factor) (SF)
DE   (Hepatopoietin A).
GN   Name:HGF; Synonyms:HPTA;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   MEDLINE=91340155; PubMed=1831432; DOI=10.1016/0378-1119(91)90080-U;
RX   Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;
RT   "Organization of the human hepatocyte growth factor-encoding gene.";
RN   [2]
RP   MEDLINE=9125062; PubMed=2145836;
RX   Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa T., Asami O.,
RA   Hagiya M., Nakamura T., Shimizu S.;
RT   "Isolation and expression of cDNA for different forms of hepatocyte
RT   growth factor from human leukocyte.";
RN   [3]
RP   MEDLINE=9006676; PubMed=2511289; DOI=10.1038/342440a0;
RX   Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimonishi M.,
RA   Sugimura A., Tashiro K., Shimizu S.;
RT   "Molecular cloning and sequence analysis of cDNA for human hepatocyte
RT   growth factor.";
RN   [4]
RP   MEDLINE=9120041; PubMed=1826653;
RX   Miyazawa K., Kitamura A., Naka D., Kitamura N.;
RT   "An alternatively processed mRNA generated from human hepatocyte
RT   growth factor gene.";
```

- RL Eur. J. Biochem. 197;15-22(1991).
- RN [6]
- RA SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 583-592.
- RC TISSUE-lung fibroblast;
- RX PubMed=1824873;
- RA Rubin J.S., Chan A.M.-L., Bottaro D.P., Burgess W.H., Taylor W.G.,
- RA Cech A.C., Hirschfield D.W., Wong J., Miki T., Finch P.W.,
- RA Aaronson S.A.;
- RT "A broad-spectrum human lung fibroblast-derived mitogen is a variant
- RT of hepatocyte growth factor";
- RL Proc. Natl. Acad. Sci. U.S.A. 88:415-419(1991).
- RN [7]
- RP SEQUENCE FROM N.A. (ISOFORM 1).
- RC TISSUE=Embryonic fibroblast;
- RX MEDLINE=91334393; PubMed=1831266;
- RA Weidner K.M., Arakaki N., Hartmann G., Vandekekerhove J., Weingart S.,
- RA Riederer H., Fonatsch C., Tsubouchi H., Hishida T., Daikuhara Y.,
- RA Birnmeier W.;
- RT "Evidence for the identity of human scatter factor and human
- RT hepatocyte growth factor";
- RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005(1991).
- RN [8]
- RP SEQUENCE FROM N.A. (ISOFORM 4).
- RX PubMed=1720571;
- RA Chan A.M.-L., Rubin J.S., Bottaro D.P., Hirschfield D.W., Chened M.,
- RA Aaronson S.A.;
- RT "Identification of a competitive HGF antagonist encoded by an
- RT alternative transcript";
- RL Science 254:1382-1385(1991).
- RN [9]
- RP SEQUENCE FROM N.A. (ISOFORM 2), AND MUTAGENESIS OF ARG-494.
- RX MEDLINE=93087571; PubMed=1280830;
- RA Hartmann G., Naldini L., Weidner K.M., Sachs M., Vigna E.,
- RA Comoglio P.M., Birnmeier W.;
- RT "A functional domain in the heavy chain of scatter factor/hepatocyte
- RT growth factor binds the c-Met receptor and induces cell dissociation
- RT but not mitogenesis";
- RL Proc. Natl. Acad. Sci. U.S.A. 89:11574-11578(1992).
- RN [10]
- RP SEQUENCE FROM N.A. (ISOFORM 6).
- RX MEDLINE=96278713; PubMed=8662798; DOI=10.1074/jbc.271.22.13110;
- RA Cioce V., Csaky K.G., Chan A.M.-L., Bottaro D.P., Taylor W.G.,
- RA Jensen R., Aaronson S.A., Rubin J.S.;
- RT "Hepatocyte growth factor (HGF)/NK1 is a naturally occurring
- RT HGF/scatter factor variant with partial agonist/antagonist activity";
- RL J. Biol. Chem. 271:13110-13115(1996).
- RN [11]
- RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LYS-304 AND TYR-330.
- RA Riederer M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
- RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
- RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
- RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
- RT of Genome Sciences, Seattle, WA (URL: <http://lepp.gs.washington.edu>).";
- RL Submitted (FEB-2003) to the EMBL/GenBank/DBS databases.
- RN [12]
- RP SEQUENCE FROM N.A.
- RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
- RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
- RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
- RA Wyllie G.A., Sekhon M., Becker M.C., O'Laughlin M.W., Schaller M.E.,
- RA Fowell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
- RA Van Hurn A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
- RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
- RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
- RA Kozlowski-Reilly A., Leonard S., Kohling T., Rock S.M.,
- RA Tin-William A.-M., Abbott A., Minx P., Maupin R., Stromatt C.,
- RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
- RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Splich L.,
- RA Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,
- RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
- RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,
- RA Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
- RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
- RA Baertsch R.A., Brent M.R., Keibler E., Flieck P., Bock P., Suyama M.,
- RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
- RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
- RA Waterston R.H., Wilson R.K.;
- RT "The DNA sequence of human chromosome 7.";
- RL Nature 424:157-164(2003).
- RN [13]
- RP SEQUENCE FROM N.A. (ISOFORMS 5 AND 6).
- RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
- RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
- RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
- RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
- RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
- RA Diatchenko L., Martuna K., Farmer A.A., Rubin G.M., Hong L.,
- RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
- RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinini P., Prange C.,
- RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
- RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatirne P.H.,
- RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
- RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
- RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
- RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
- RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
- RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
- RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
- RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
- RT "Generation and initial analysis of more than 15,000 full-length human
- RT and mouse cDNA sequences";
- RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
- RN [14]
- RP SEQUENCE OF 1-208 AND 249-695 FROM N.A. (ISOFORM 1).
- RX MEDLINE=91369928; PubMed=1832556;
- RA Miyazawa K., Kitamura A., Kitamura N.;
- RT "Structural organization and the transcription initiation site of the
- RT human hepatocyte growth factor gene";
- RL Biochemistry 30:9170-9176(1991).
- RN [15]
- RP SIGNAL SEQUENCE CLEAVAGE SITE.
- RX MEDLINE=91207365; PubMed=1826837;
- RA Yoshiyama Y., Arakaki N., Naka D., Takahashi K., Hiroto S., Kondo J.,
- RA Nakayama H., Gohda E., Kitamura N., Tsubouchi H., Ishii T.,
- RA Hishida T., Daikuhara Y.;
- RT "Identification of the N-terminal residue of the heavy chain of both
- RT native and recombinant human hepatocyte growth factor";
- RL Biochem. Biophys. Res. Commun. 175:660-667(1991).
- RN [16]
- RP CARBOHYDRATE LINKAGE SITE. THR-476.
- RX MEDLINE=93129192; PubMed=1482348;
- RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
- RA Nakamura T., Shimizu S.;
- RT "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
- RT on the alpha chain";
- RL Biochem. Biophys. Res. Commun. 189:1329-1335(1992).
- RN [17]
- RP MUTAGENESIS.
- RX MEDLINE=92331602; PubMed=1321034;
- RA Loker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins K.A.,
- RA Baker J.B., Godowski P.J.;
- RT "Structure-function analysis of hepatocyte growth factor:
- RT identification of variants that lack mitogenic activity yet retain
- RT high affinity receptor binding";
- RL EMBO J. 11:2503-2510(1992).
- RN [18]
- RP STRUCTURE BY NMR OF 31-127.
- RX MEDLINE=9815423; PubMed=9493272; DOI=10.1016/S0969-2126(98)00012-4;
- RA Zhou H., Mazziola M.J., Kaufman J.D., Stahl S.J., Wingfield P.T.,
- RA Rubin J.S., Bottaro D.P., Byrd R.A.;
- RT "The solution structure of the N-terminal domain of hepatocyte growth
- RT factor reveals a potential heparin-binding site";
- RL Structure 6:109-116(1998).
- RN [19]
- RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.

RA	MEDLINE=99036658; PubMed=9817840; DOI=10.1016/S0969-2126(98)00138-5; Utesch M., Lokker N.A., Godowski P.J., de Vos A.M.;
Query Match	99.4%; Score 2563.5; DB 1; Length 728;
Best Local Similarity	98.7%; Pred. No. 28-185;
Matches 441; Conservative	1; Mismatches 0; Indels 5; Gaps 1
QY	1 ERKRNTTTFEPKSAKLTLLIKIDPALIKITKKVNTADOCANRCTRNKGIPLFCCKAFVDPK 60
DB	32 QKRKRNTHTEFFKSKATLLIKIDPALIKITKKVNTADOCANRCTRNKGLPFTCKAFVDPK 91
QY	61 ARKOCLEPFPNMSGSVKKEPFEHEPDLLENKDYINRCIIIGKRSYKGTYSITKSGIKOP 120
DB	92 ARKOCLEPFPNMSGSVKKEPFEHEPDLLENKDYINRCIIIGKRSYKGTYSITKSGIKOP 151
QY	121 WSSMIPIHEH-----SYRKDIOENYCRNPRGEGGPMWCTSNPEVRYEVCIDIPOCSVEVC 175
DB	152 WSSMIPIHEHSFLPSYRGKDIQENYCRNPRGEGGPMWCTSNPEVRYEVCIDIPOCSVEVC 211
QY	176 MTCNGESYRGLMDHTESGKICQRMWHQTPHRAKFLPERYPDKGPDNDYCRNPDGPRPC 235
DB	212 MTCNGESYRGLMDHTESGKICQRMWHQTPHRAKFLPERYPDKGPDNDYCRNPDGPRPC 271
QY	236 YTLDPHTWEYCAITQCADNTMNDVDVPLETECCIOGGEGRGVNTIWNIGPCORWDS 295
DB	272 YTLDPHTWEYCAITQCADNTMNDVDVPLETECCIOGGEGRGVNTIWNIGPCORWDS 331
QY	296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFPTDPNIRIVGCSQIPLNCDSHGQDC 355
DB	332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFPTDPNIRIVGCSQIPLNCDSHGQDC 391
QY	356 YRGNGKNYMGNISQTRSGLTCSMDMKMEDLHRHIFWEPSDKLNENYCRNPDDAHGPW 415
DB	392 YRGNGKNYMGNISQTRSGLTCSMDMKMEDLHRHIFWEPSDKLNENYCRNPDDAHGPW 451
QY	416 CYTGNPLIPWDYCPISRCBGDTTPITV 442
DB	452 CYTGNPLIPWDYCPISRCBGDTTPITV 478
RESULT 2	
Q867B7	PRELIMINARY; PRT; 730 AA.
AC	Q867B7;
DT	01-JUN-2003 (TREMBlrel. 24, Created)
DT	01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT	05-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE	Hepatocyte growth factor.
GN	Name=HGF;
OS	Canis familiaris (Dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX	NCBI_TaxID=9615;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Beagle;
RX	MEDLINE=22844761; PubMed=12963274; DOI=10.1016/S0165-2427(03)00118-1;
RA	Mayake M., Saze K., Yaguchi T., Wang J., Suzuta Y., Haga Y.,
RT	Takahashi S.Y., Yamamoto Y., Iwabuchi S.;
RT	"Canine hepatocyte growth factor: molecular cloning and
RT	characterization of the recombinant protein.";
RL	Vet. Immunol. Immunopathol. 95:135-143(2003).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Liso A.T., Chien M.B., London C.A.;
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: Belongs to peptidase family S1.
DR	EMBL; AB090353; BACS7560.1; -
DR	EMBL; AY543632; AAS48570.1; -
DR	HSSP; P14210; IGMN.
DR	MEROPS; S01.982; -
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.
DR	GO; GO:0008233; F:peptidase activity; IEA.

Query Match	Best Local Similarity	94.0%	Score 2424.5	DB 2	Length 730
Matches	411	Conservative 19	Mismatches 12	Indels 5	Gaps 1
QY	1	ERKRNTIHEFKSAKTLIKIDPAKIKTKKNTADOCANRCTRNKGIPLFCKAFVFDK	60		
Db	32	QKKRRNTIHEFKSAKTLIKEDPLKIKTKKNTADOCANRCINNKGIPLFCKAFVFDK	91		
QY	61	ARKCIMEPFPMSGSVKKEFGHEFDLYENKDYIINCIIGKRSYKGVSTIKSGIKOOP	120		
Db	92	ARKCIMEPFPMSGSVKKEFGHEFDLYENKDYIINCIIGKGSYKGVSTIKSGIKOOP	151		
QY	121	WSMI PHEH-----SYRGKDIOENYCRNPRGEGPWCFTSNPEVRYEVCDIPOCSEVEC	175		
Db	152	WNSMI PPHSHSLPSSYRKDKIOENYCRNPRGEGPWCFTSNPEVRYEVCDIPOCSEVVC	211		
QY	176	MTNGESTYRGLMDHTESGKICQMDHQTPIHKKFLPEFYPDKGPDONTCRNPDGPRPWC	235		
Db	212	MTNGESYRGMDDHTESGKICQMDHQTPIHKKFLPEFYPDKGPDONTCRNPDGKPRPWC	271		
QY	236	YTLDPHTFWECAIKTCADNTMNDTDVLELTTECIQGGEGEGRGVNTIMNGIPCORPMS	295		
Db	272	YTLDPHTFWECAIKMCHASTMNDTDVLELTTECIQGGEGEGRGVNTIMNGVPCQRMDS	331		
QY	296	QYPEHMDPTPNPFCKDLRENYCRNPDSESIPMCFTTDPNIRIVGCSQIPNCDMSHGDC	355		
Db	332	QYPIQHDPTPNPFCKDLRENYCRNPDGABSPMCTTDPNIRIVGCSQIPKCDVSSGDC	391		
QY	356	YRGNGKNYMGNLISOTRSGLTCSMDKNMEDLHRHIFWEPDASKINENYCRNDDDAHGPW	415		
Db	392	YRGNGKNYMGNLISOTRSGLTCSMDKNMEDLHRHIFWEPDASKINENYCRNDDDAHGPW	451		
QY	416	CYTGNDPLIPWDYCPISRCGCTTPPIV 442			
Db	452	CYTGNDPLIPWDYCPISRCGCTTPPIV 478			

RESULT 3

Q76BS1 PRELIMINARY; PRT. 730 AA.

AC Q76BS1.

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE Hepatocyte growth factor.

OS Name=ngf;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yamaji D., Kimura K., Matanabe A., Makondo K., Saito M.,  
 RL Submitted (May-2003) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL; AB110822; BAD02475.1; -.  
 DR HSSP; P08519; IKTV.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR011359; HGF\_MSTL.  
 DR InterPro; IPR000001; Kirtingle.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR003609; Pan\_app.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR Pfam; PF00051; Kirtingle; 4.  
 DR Pfam; PF00024; PAN; 1.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PIRSF; PIRSF001152; HGF\_MSTL; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00018; KRINGLE.  
 DR ProDom; PD000395; Kirtingle; 4.  
 DR SMART; SM00130; KR; 4.  
 DR SMART; SM00473; PAN\_AP; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00021; KRINGLE\_1; 4.  
 DR PROSITE; PS50070; KRINGLE\_2; 4.  
 DR PROSITE; PS50948; PAN; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; Kirtingle; Protease; Serine protease.  
 DR Hydrolase; Kirtingle; Protease; Serine protease.  
 KW Kirtingle; Protease; Serine protease.  
 SO SEQUENCE 730 AA; 83357 MW; E39D653B0A85F49B CRC64;

Query Match 93.8%; Score 2418.5; DB 2; Length 730;  
 Best Local Similarity 91.5%; Pred. No. 1.8e-174;  
 Matches 409; Conservative 22; Mismatches 11; Indels 5; Gaps 1;

QY 1 ERKRRNTIHEPKSAKTLIKIDPALKIKTKKVTADQCANRCTRNKGLPTCKAFVDPK 60  
 DB 32 QKKRRNTIHEPKSAKTLIKIDPALKIKTKKVTADQCANRCTRNKGLPTCKAFVDPK 91

QY 61 ARKQCLWPFNPMSSGVKKEFGHEFDLYENKDYINNCIIGKRSYKGYTSITKSGIKCP 120  
 DB 92 ARKQCLWPFNPMSSGVKKEFGHEFDLYENKDYINNCIIGKRSYKGYTSITKSGIKCP 151

QY 121 WSSMTIPEH-----SYRGKDLQENYCRNPRGEGGPMCTSNPEVREYECDIPOCSEVVC 175  
 DB 152 WSSMTIPEHISFLPSSTRGKDLQENYCRNPRGEGGPMCTSNPEVREYECDIPOCSEVVC 211

QY 176 MTCNGESYRGKDLQENYCRNPRGEGGPMCTSNPEVREYECDIPOCSEVVC 235  
 DB 212 MTCNGESYRGKDLQENYCRNPRGEGGPMCTSNPEVREYECDIPOCSEVVC 271

QY 236 YLLDPTHTREYCAIKTCANNTWMDVPLETTECTIOGEGSIRGYNTIWNGLPCQRWMS 295  
 DB 272 YLLDPTHTREYCAIKTCANNTWMDVPLETTECTIOGEGSIRGYNTIWNGLPCQRWMS 331

QY 296 QYRPHEDMTPEPNPKCDLRENYCRNPDGSESPMCTTDNINIVGYSQIPNCMDSHGQDC 355  
 DB 332 QYRPHEDMTPEPNPKCDLRENYCRNPDGSESPMCTTDNINIVGYSQIPNCMDSHGQDC 391

QY 356 YRNGNGKNVGNLSQTSRGLTCSWMDKQMEDLHRHIFWEPDASKLQENYCRNPDGDAHGPW 415  
 DB 392 YRNGNGKNVGNLSQTSRGLTCSWMDKQMEDLHRHIFWEPDASKLQENYCRNPDGDAHGPW 451

QY 416 CYTGNPLIWDYICPISRCGDTPTIV 442

DB 452 CYTGNPLIWDYICPISRCGDTPTIV 478

RESULT 4  
 Q9BH09 PRELIMINARY; PRT; 728 AA.  
 AC Q9BH09;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hepatocyte growth factor HGF.  
 GN Name=HGF;  
 OS Fells silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felle.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Kobayashi Y., Nakamura N., Ishizaka T., Maeda K., Ohno K.,  
 RA Tsujimoto H.;  
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Miyake M., Yaguchi T., Saze K., Suzuta Y., Wang J., Okazaki M.,  
 RA Haga Y., Yamamoto Y., Takahashi S., Iwabuchi S.;  
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL; AB046610; BAB21499.1; -.  
 DR EMBL; AB080187; BAC10545.1; -.  
 DR HSSP; P14210; IGMN.  
 DR MEROPS; S01.982; -.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR011359; HGF\_MSTL.  
 DR InterPro; IPR000001; Kirtingle.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR003609; Pan\_app.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR Pfam; PF00051; Kirtingle; 4.  
 DR Pfam; PF00024; PAN; 1.  
 DR PIRSF; PIRSF001152; HGF\_MSTL; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00018; KRINGLE.  
 DR ProDom; PD000395; Kirtingle; 4.  
 DR SMART; SM00130; KR; 4.  
 DR SMART; SM00473; PAN\_AP; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00021; KRINGLE\_1; 4.  
 DR PROSITE; PS50070; KRINGLE\_2; 4.  
 DR PROSITE; PS50948; PAN; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; Kirtingle; Protease; Serine protease.  
 DR Hydrolase; Kirtingle; Protease; Serine protease.  
 KW Kirtingle; Protease; Serine protease.  
 SO SEQUENCE 728 AA; 83067 MW; 8D7F4A333D1B190A CRC64;

Query Match 93.6%; Score 2414.5; DB 2; Length 728;  
 Best Local Similarity 91.5%; Pred. No. 3.7e-174;  
 Matches 409; Conservative 21; Mismatches 12; Indels 5; Gaps 1;

QY 1 ERKRRNTIHEPKSAKTLIKIDPALKIKTKKVTADQCANRCTRNKGLPTCKAFVDPK 60  
 DB 30 QKKRRNTIHEPKSAKTLIKIDPALKIKTKKVTADQCANRCTRNKGLPTCKAFVDPK 89

QY 61 ARKQCLWPFNPMSSGVKKEFGHEFDLYENKDYINNCIIGKRSYKGYTSITKSGIKCP 120  
 DB 90 ARKQCLWPFNPMSSGVKKEFGHEFDLYENKDYINNCIIGKRSYKGYTSITKSGIKCP 149

QY 121 WSSMTIPEH-----SYRGKDLQENYCRNPRGEGGPMCTSNPEVREYECDIPOCSEVVC 175



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Db 150 WNSMIPHEHSFLPSSIRGKLOENYCNPRGEGGPMCFPSNBEVREVCDDIQCESEVC
Qy 176 MTCNGESYRGIMDHTESSGKICORWDHQPPIRHHKFLPERYPDKGFDDNYCNPDPGPRPMC
Db 210 MTCNGESYRPMHHTSSGKICORWDHQPPIRHHKFLPERYPDKGFDDNYCNPDPGPRPMC
Qy 236 YTLDPHTREMYCAIKTCADNTMDTVDVPLETTECICQGGEGYRGVTNTVINGIPCORWDS
Db 270 YTLDPHTREMYCAIKTCADNTMDTVDVPLETTECICQGGEGYRGVTNTVINGIPCORWDS
Qy 296 QYEHEDMPENKCDLRENYCRNPDGSEPMCFPTDPIRIGYCSQIPNCDMSHGDC 355
Db 330 QYEHEDMPENKCDLRENYCRNPDGSEPMCFPTDPIRIGYCSQIPNCDMSHGDC 389
Qy 356 YRGNGKNYKGNLTSQTSRGLTCSMMWDMEDLHRIHIEWEPASKLINENYCRNPDGDAHGP 415
Db 390 YRGNGKNYKGNLTSQTSRGLTCSMMWDMEDLHRIHIEWEPASKLINENYCRNPDGDAHGP 449
Qy 416 CYTGNPLIPWDYCPISRCGEGDTPTIV 442
Db 450 CYTGNPLIPWDYCPISRCGEGDTPTIV 476

RESULT 5
ID 08C9G5 PRELIMINARY; PRT; 728 AA.
AC 08C9G5;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630060C16 product:hepatocyte growth factor, full
DE insert sequence.
GN Name:Hgf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid:10090;
RN 1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN 12)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN 13)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The PANTOM Consortium;
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN 14)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN 15)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
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RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunai T., Taahiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN 16)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL: AK042121; BAC31175.1; -.
DR HSSP: P14210; 1GMN.
DR MCD; MG1:96079; Hgf.
DR GO; GO:0008283; P:cell proliferation; IDA.
DR GO; GO:0009092; P:cellular morphogenesis; IDA.
DR InterPro; IPR011359; HGF_MST1.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003609; PAN.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PIRSF001152; HGF_MST1; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRODOM; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_Ap; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS00070; KRINGLE_2; 4.
DR PROSITE; PS00948; PAN; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR Kowolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 728 AA; 82990 MW; 8D5258DF3BCF3545 CRC64;

Query Match 92.0%; Score 2371.5; DB 2; Length 728;
Best local Similarity 89.9%; Pred 23.6-171;
Matches 402; Conservative 21; Mismatches 19; Indels 5; Gaps 1;

Qy 1 ERKRNTIHEFKSAKTLTIKIDPALKI KTKKVTNADQCANRCTRNGLPFTCKAFVDPK 60
Db 33 OKRRNTIHEFKSAKTLTIKIDPALKI KTKKVTNADQCANRCTRNGLPFTCKAFVDPK 92
Qy 61 AKQCLMPFPNMSGYKKEFGHEPDLNENKYINNCIIGKRSYKGYSTIRKSGIKCOP 120
Db 93 SKRRKYWPFPNMSGYKKEFGHEPDLNENKYINNCIIGKRSYKGYSTIRKSGIKCOP 152
Qy 121 WNSMIPHEH-----SYRGKLOENYCRNPRGEGGPMCFPSNBEVREVCDDIQCESEVC 175
Db 153 WNSMIPHEHSFLPSSIRGKLOENYCRNPRGEGGPMCFPSNBEVREVCDDIQCESEVC 212
Qy 176 MTCNGESYRGIMDHTESSGKICORWDHQPPIRHHKFLPERYPDKGFDDNYCNPDPGPRPMC 235
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Db      213  MTCNSESRYGPMWHTSGKTCQRMDOQTPEHRKFLPERYPDXGFPDNYCRNPDGKPRPWC 272
Oy      226  YTLDDHTWMEVCAITCCADNTMNDPVPETTECTOGGEGRGVNTMNICORRDS 295
Db      273  YTLDDHTWMEVCAITCCADNTMNDPVPETTECTOGGEGRGVNTMNICORRDS 332
Oy      296  QYPHEMDTPENFKCKDLRENYCRNPDGSESPWCTTTPNIRVGYCSQIPNCDSHGDC 355
Db      333  QYPHMDITPENFKCKDLRENYCRNPDGSESPWCTTTPNIRVGYCSQIPNCDSHGDC 392
Oy      356  YRGNKNTYNGNISQTRSGITCSMDKNMEDLHRHIFWEPDASKLMENTCRNDDAHGFW 415
Db      393  YRGNKNTYNGNISQTRSGITCSMDKNMEDLHRHIFWEPDASKLMENTCRNDDAHGFW 452
Oy      416  CYTGNPLIPMDYCPISRCGSDTPTTV 442
Db      453  CYTGNPLIPMDYCPISRCGSDTPTTV 479

RESULT 6
HGF_MOUSE
ID_HGF_MOUSE  STANDARD; PRT; 728 AA.
AC  Q08048; Q61662; Q64007;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Hepatocyte growth factor precursor (Scatter factor) (SF)
    (Hepatopoietin A).
GN  Name=Hgf;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND SEQUENCE OF 496-504.
RC  TISSUE=Mammary Fibroblast;
RX  MEDLINE=94183257; PubMed=815822;
RA  Sasaki M., Nishio M., Sasaki T., Enami J.;
RT  "Identification of mouse mammary fibroblast-derived mammary growth
    factor as hepatocyte growth factor.";
RL  Biochem. Biophys. Res. Commun. 199; 772-779 (1994).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Liver;
RX  MEDLINE=94363381; PubMed=8081873;
RA  Lee C.C., Kozak C.A., Yamada K.M.;
RT  "Structure, genetic mapping, and expression of the mouse Hgf/scatter
    factor gene.";
RL  Cell Adhes. Commun. 1:101-111 (1993).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Liver;
RX  MEDLINE=94060105; PubMed=8241272; DOI=10.1016/0167-4781(93)90159-B;
RA  Liu Y., Michalopoulos G.K., Zarnegar R.;
RT  "Molecular cloning and characterization of cDNA encoding mouse
    hepatocyte growth factor.";
RL  Biochim. Biophys. Acta 1216:299-303 (1993).
CC  -I- FUNCTION: HGF is a potent mitogen for mature parenchymal
    hepatocyte cells, seems to be an hepatotrophic factor, and acts as
    growth factor for a broad spectrum of tissues and cell types. It
    has no detectable protease activity.
CC  -I- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
    disulfide bond.
CC  -I- ALTERNATIVE PRODUCTS:
    Event=Alternative splicing; Named isoforms=2;
    Name=Long;
    IsoId=Q08048-1; Sequence=Displayed;
    Name=Short;
    IsoId=Q08048-2; Sequence=WSP_005408;
CC  -I- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
    subfamily.
CC  -I- SIMILARITY: Contains 4 kringle domains.

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CC  -I- SIMILARITY: Contains 1 PAN domain.
-----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC  or send an email to license@ebi.ac.uk).
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DR  EMBL; D10212; BAA01064.1; -
DR  EMBL; D10213; BAA01065.1; -
DR  EMBL; S71816; BAB31855.1; -
DR  EMBL; X72307; CAAS1054.1; ALT_INIT.
DR  PIR; JC2117; A60185.
DR  HSSP; P14210; 1BHT.
DR  MEROPS; S01.982; -.
DR  MGD; MGI:96079; Hgf.
DR  GO; GO:0008283; P:cell proliferation; IDA.
DR  GO; GO:0009042; P:cellular morphogenesis; IDA.
DR  InterPro; IPR000001; Kringle.
DR  InterPro; IPR003014; PAN.
DR  InterPro; IPR003609; Pan_app.
DR  InterPro; IPR009003; pepc_Ser_Cys.
DR  InterPro; IPR001254; peptidase_S1.
DR  InterPro; IPR001314; peptidase_S1A.
DR  Pfam; PF00051; Kringle; 4.
DR  Pfam; PF00024; PAN; 1.
DR  Pfam; PF00089; Trypsin; 1.
DR  Pfam; PF000152; HGF_MST1; 1.
DR  PRINTS; PR00722; CHYMOTRYPSIN.
DR  PRINTS; PR00018; KRINGLE.
DR  ProDom; PD000395; Kringle; 4.
DR  SMART; SM00130; KR; 4.
DR  SMART; SM00473; PAN_AP; 1.
DR  SMART; SM00020; TRYP_Ser; 1.
DR  PROSITE; PS00021; KRINGLE_1; 4.
DR  PROSITE; PS50070; KRINGLE_2; 4.
DR  PROSITE; PS50948; PAN; 1.
DR  PROSITE; PS50240; TRYPSIN_DOM; 1.
KW  Alternative splicing. Direct protein sequencing. Glycoprotein;
KW  Growth factor; Kringle; Pyroglutamate carboxylic acid; Repeat;
KW  Serine protease homolog; Signal.
FT  SIGNAL 1 32
FT  CHAIN 33 495
FT  CHAIN 496 728
FT  MOD_RES 33 33
FT  DOMAIN 38 124
FT  DOMAIN 129 207
FT  DOMAIN 212 289
FT  DOMAIN 306 384
FT  DOMAIN 392 470
FT  DOMAIN 496 728
FT  DISULFID 71 97
FT  DISULFID 75 85
FT  DISULFID 488 607
FT  CARBOHYD 295 295
FT  CARBOHYD 403 403
FT  CARBOHYD 569 569
FT  CARBOHYD 656 656
FT  VARSPPLIC 163 167
FT  CONFLICT 344 344
FT  CONFLICT 479 479
FT  CONFLICT 564 564
SQ  SEQUENCE 728 AA; 82944 MW; A0381FC497534328 CRC64;

Query Match          91.9%; Score 2370.5; DB 1; Length 728;
Best Local Similarity 89.9%; Pred. No. 7.8e-171;
Matches 402; Conservative 21; Mismatches 19; Indels 5; Gaps 1;
Oy      1  ERKRNTIHFPKSAKTLIKIDIPALKIKTKKVTADOCANCRTRNKGLPFTCKAFVFDK 60

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Db      33  QKRRNTLHEFKKSATTTLTKEPDLKIKTKKYNASDECANRRIIRNGPFTTCKAFVFDK 92
Qy      61  ARKQCLMPFPNSNSGCVKKEFGHEPDLYENKDYIRNCIIIGKRSYGTVAITSGIKCOP 120
Db      93  SRKRCYWPFPNSNSGCVKKEFGHEPDLYENKDYIRNCIIIGKRSYGTVAITSGIKCOP 152
Qy      121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEGGPMCFSTSNPEVRYEVCIDIQCSBEVC 175
Db      153 WNSMIDHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCFSTSNPEVRYEVCIDIQCSBEVC 212
Qy      176 MTCNGSSYSGKLMHTSSGKTCQRMWDTQPRHAKFLPERYDVKXGPDNDYCNPNPGQPRPWC 235
Db      213 MTCNGSSYSGKPMHTSGKTCQRMWDTQPRHAKFLPERYDVKXGPDNDYCNPNPGQPRPWC 272
Qy      236 YTLDPHTREYCAIKTCADNTAMDTPVPLETTECICQOQSGYGTVAITNGI PCORMDS 295
Db      273 YTLDPHTREYCAIKTCADNTAMDTPVPLETTECICQOQSGYGTVAITNGI PCORMDS 332
Qy      296 QYPHEHDMTPENFKCDLRENYCRNPDGSESPWCFTTDPNIRVYCSQI PCNCDMSHGQDC 355
Db      333 QYPHKADITPENFKCDLRENYCRNPDGSESPWCFTTDPNIRVYCSQI PCNCDMSHGQDC 392
Qy      356 YRNGNGKYNMGNTLSQTSGLTCSMWDKXMDLHRIHMEPDAKLANENYCRNPDGDAHGPW 415
Db      393 YRNGNGKYNMGNTLSQTSGLTCSMWDKXMDLHRIHMEPDAKLANENYCRNPDGDAHGPW 452
Qy      416 CYTGNPLIPMDYCPISRCGDTPTTY 442
Db      453 CYTGNPLIPMDYCPISRCGDTPTTY 479

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## RESULT 7

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HGF_RAT ID HGF_RAT STANDARD; PRT; 728 AA.
AC P17545;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hepatocyte growth factor precursor (Scatter factor) (SF)
DE (Hepatopoietin A).
GN Name=Hgf;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Miscar; TISSUE=Liver;
RX MEDLINE=90222197; PubMed=2139229;
RA Toshiro K., Hagiya M., Nishizawa T., Seki T., Shimomishi M.,
RA Shimizu S., Nakamura T.;
RT "Deduced primary structure of rat hepatocyte growth factor and
RT expression of the mRNA in rat tissues."
RT Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar; TISSUE=Liver;
RX MEDLINE=91031482; PubMed=2146117;
RA Okajima A., Miyazawa K., Kitamura N.;
RA "Primary structure of rat hepatocyte growth factor and induction of
RT its mRNA during liver regeneration following hepatic injury."
RT Eur. J. Biochem. 193:375-381(1990).
CC -I- FUNCTION: HGF is a potent mitogen for mature parenchymal
CC hepatocyte cells, seems to be an hepatotrophic factor, and acts as
CC growth factor for a broad spectrum of tissues and cell types. It
CC has no detectable protease activity.
CC -I- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
CC disulfide bond.
CC -I- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC subfamily.
CC -I- SIMILARITY: Contains 4 kringle domains.
CC -I- SIMILARITY: Contains 1 PAN domain.

```

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CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D90102; BAA14133.1; -
DR EMBL: X54400; CA38266.1; -
DR PIR: A35644; A35644.
DR HSP: P14210; 1BHT.
DR MEROPS: S01.978; -.
DR RGD: 2794; Hgf.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR InterPro: IPR01254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00051; Kringle; 4.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; Trypsin; 1.
DR PIRSF: PIRSF001152; HGF_MST1; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR ProDom: PD000395; Kringle; 4.
DR SMART: SM00130; KR; 4.
DR SMART: SM00473; PAN_Ap; 1.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS00021; KRINGLE_1; 4.
DR PROSITE: PS50070; KRINGLE_2; 4.
DR PROSITE: PS50948; PAN; 1.
DR PROSITE: PS50240; TRYP_SIN_DOM; 1.
KW Direct protein sequencing; Glycoprotein; Growth factor; Kringle;
KW Pyroliidone carboxylic acid; Repeat; Serine protease homolog; Signal.
FT SIGNAL 1 32
FT CHAIN 33 495
FT CHAIN 496 728
FT MOD_RES 33 33
FT DOMAIN 38 124
FT DOMAIN 129 207
FT DOMAIN 212 289
FT DOMAIN 305 384
FT DOMAIN 392 470
FT DOMAIN 496 728
FT DISULFID 71 97
FT DISULFID 75 85
FT DISULFID 488 607
FT CARBOHYD 295 295
FT CARBOHYD 403 403
FT CARBOHYD 469 569
FT CARBOHYD 569 656
SQ SEQUENCE 728 AA; 82905 MW; 3E0BF1F96ADCEDFF CRC64;

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Query Match 91.6%; Score 2363.5; DB 1; Length 728;

Best Local Similarity 89.3%; Pred. No. 2,6e-170; Mismatches 20; Indels 5; Gaps 1;

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Qy      1  ERKRRNTLHEFKKSATTTLTKEPDLKIKTKKYNASDECANRRIIRNGPFTTCKAFVFDK 60
Db      33  QKRRNTLHEFKKSATTTLTKEPDLKIKTKKYNASDECANRRIIRNGPFTTCKAFVFDK 92
Qy      61  ARKQCLMPFPNSNSGCVKKEFGHEPDLYENKDYIRNCIIIGKRSYGTVAITSGIKCOP 120
Db      93  SRKRCYWPFPNSNSGCVKKEFGHEPDLYENKDYIRNCIIIGKRSYGTVAITSGIKCOP 152
Qy      121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEGGPMCFSTSNPEVRYEVCIDIQCSBEVC 175
Db      153 WNSMIDHEHSFLPSSYRGKDLQENYCRNPRGEGGPMCFSTSNPEVRYEVCIDIQCSBEVC 212

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Qy	176	MTCNSESXRGIMDHTHESGTCQRMWQHOTHPRHFLPERYDDKGFDDNNCGNPDGQGRPMC	235
Db	213	MTCNESSTXRGPMDDHTHESGTCQRMWQDQTPHRHFLPERYDDKGFDDNNCGNPDGKPRPMC	272
Qy	236	YTLDPHTRMWYCAIKTCADNTMNDIVDPLPETTECIGQGGEGYRGVTNTIWNIGIPCQRWDS	295
Db	273	YTLDEPDTPMWYCAIKKCAHSAVNETDVPMETTECIGKQGGYRGVTNTIWNIGIPCQRWDS	332
Qy	256	QYPHEDHMPPEMPFKCDLPENYCRNPDGSESPPMCFITDPMIRXGYSQIPNCMSHGQDC	355
Db	333	QYPHKHDTIPENPKCDLPENYCRNPDGASPPMCFITDPMIRXGYSQIPKCVSSGQDC	392
Qy	356	YRGNGKNVYGNLSQTSRGLTCSMWDMKMDLHRHIFWEPDASKLNNENYCRNPDDDAHGPW	415
Db	393	YRGNGKNVYGNLSKTSRGLTCSMWDMKMDLHRHIFWEPDASKLTNXYCGRNPDDAHGPW	452
Qy	416	CYTGNDPLMPWDCPISRCGEGDTPTTV	442
Db	453	CYTGNDPLVWDCPISRCGEGDTPTTV	479

## RESULT 8

ID	Q90978	PRELIMINARY;	PRT;	726 AA.
AC	Q90978	Q90866;		
DT	01-JAN-1998	(TREMBLrel. 05, Created)		
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	Hepatocyte growth factor /scatter factor.			
GN	Name:HGF/SF;			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;			
OC	Athysanura; Aves; Neognathae; Galliformes; Gallinae; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
FX	MEDLINE=96029010; PubMed=7554499;			
RA	Thery C., Shupe M.J., Batley S.J., Stern C.D., Cherard E.;			
RT	"Expression of HGF/SF, HGF/MSP and c-met suggests new functions			
RT	during early chick development.";			
RL	Dev. Genet. 17:90-101(1995).			
CC	-1- SIMILARITY: Belongs to peptidase family S1.			
DR	EMBL, X64045; CAAS8864.1; -.			
DR	PIR, I51285; I51285.			
DR	HSSP, P14210; IGMN.			
DR	GO; GO:004263; F:chymotrypsin activity; IEA.			
DR	GO; GO:008233; F:peptidase activity; IEA.			
DR	GO; GO:004295; F:trypsin activity; IEA.			
DR	GO; GO:006508; P:proteolysis and peptidolysis; IEA.			
DR	Pfam; PF00051; Kringle; 4.			
DR	Pfam; PF00024; PAN; 1.			
DR	Pfam; PF00089; Trypsin; 1.			
DR	PIRSF; PIRSF001152; HGF_MST1; 1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	PRINTS; PR00018; KRINGLE.			
DR	ProDom; PD000395; Kringle; 4.			
DR	SMART; SM00130; KR; 4.			
DR	SMART; SM00473; PAN_AP; 1.			
DR	SMART; SM00020; Tryp_SPC; 1.			
DR	PROSITE; PS00021; KRINGLE_1; 4.			
DR	PROSITE; PS50070; KRINGLE_2; 4.			
DR	PROSITE; PS50948; PAN; 1.			
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.			
KW	Hydrolase; kringle; protease; Serine protease.			
SC	SEQUENCE 726 AA; 82865 MW; 5BD06CFB5C40B003 CRC64;			

Query Match	78.1%	Score 204.5	DB 2	Length 725
Best Local Similarity	75.5%	Pred. No. 6.5e-144		
Matches 336	Conservative 49	Mismatches 53	Indels 7	Gaps 2

QY 3 KRRNTTHERKSAKATLLIKIDPALKTKTKKVTADOCANRCRNRKGLPTTCAPVDDKAR 62

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Db      30  KRRNLDHYKXKTGELMLLKVNKTLBVKTKLLNTTQCAKRGSRNGLSPTCKAFAYDRVT  89
Qy      63  KQCLMFPPNNSSSGVYKEBGEFDLYENKDYRNCLIGKSGSYKGTVLTITKSGIKQCPMS  122
Db      90  KRCHWLSFNSLITNGRKXKODHAFDFPEKKDYRNCLIGGAGAYKGTISITKSGIQOAWN  149
Qy     123  SMIPHEH-----SYRGKDLQENYCNPNRGEQGPNCFTNPBEVRYEVCIIPOCEEVCMT  177
Db     150  SNIPIHEHGFPLPSYVGKDLRENYCNRNPRGEBGGPMTTSPQMRHEVCIIPLCEVECMT  209
Qy     178  CNGESYRGMLDHTSESGKICQRMWHOTPHRKFLPERYPDKGFEDNYCRNPDGQPRPWCYT  237
Db     210  CNGESYRGMDHTSESGEKQRMWDLQRPHKHKRPERYPDKGFEDNYCRNPDGKFLRPMCT  269
Qy     238  LDPHTRWEXCAIKTADNTMDNTDVPLETTBECIOQGESEYRGTYVNTIIMGICPCQRMSQY  297
Db     270  LDPNTPWEECAIKTQDVGILNSTEVAETTTIOQGESEYRGTYVNTIIMGICQQRMSQF  329
Qy     298  PHEHMTPENFCKDLRENYCNRNPGASEPWCFTTDPNIRVAYCSQIPNCDSMHSQDCYR  357
Db     330  PHQHNITPENFCKDLRENYCNRNPGOSEPWCFTTDPNIRIGYCSQIPKCDVSNEDCYR  389
Qy     358  GNGKNYMGULSQTRSGLTCSMWDKNMEDLHRH--IFWEBDASKLBNYCRNPDDBAHGPW  415
Db     390  GNGKSYMGULSNTRIGLTCSTWDKNIEDLRHIIQIFREBDVSKLKNKYCRNPDDBFHGPW  449
Qy     416  CYTGNPDLIPWDYCPISRCEGDDTTPT  440
Db     450  CYTDDELIPWDYCPISRCTGDDTTPT  474

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## RESULT 5

ID	091402	PRELIMINARY;	PRT:	710 AA.
AC	Q91402;			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	Hepatocyte growth factor.			
GN	Name=HGF;			
OS	Xenopus.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;			
OC	Xenopodinae.			
OX	NCBI_TaxId=8353;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Tailbud;			
RX	MEDLINE=95567690; PubMed=7748783; DOI=10.1016/0925-4773(94)00309-B;			
RA	Nakamura H., Tashiro K., Nakamura T., Shiohawa K.			
RT	"Molecular cloning of Xenopus HGF cDNA and its expression studies in			
RT	Xenopus early embryogenesis."			
RL	Mech. Dev. 49:123-131 (1995).			
CC	-1- SIMILARITY: Belongs to peptidase family S1.			
CC	EMBL: S77422; AAB34354.2; -.			
DR	HSPF, P14210; IGMN.			
DR	MEROPS, S01.976; -.			
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.			
DR	GO; GO:0008233; F:peptidase activity; IEA.			
DR	GO; GO:0004295; F:trypsin activity; IEA.			
DR	GO; GO:0006508; F:proteolysis and peptidolysis; IEA.			
DR	Pfam; PF00051; Kringle; 4.			
DR	Pfam; PF00024; PAN; 1.			
DR	Pfam; PF00089; Trypsin; 1.			
DR	PIRSF: PIRSFO01152; HGF MS1; 1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	PRINTS; PR00018; KRINGLE.			
DR	Prodom; PD000395; Kringle; 4.			
DR	SMART; SM00130; KR; 4.			
DR	SMART; SM00473; PAN_AP; 1.			
DR	SMART; SM00020; Tryp_Sec; 1.			
DR	PROSITE; PS00021; KRINGLE_1; 4.			
DR	PROSITE; PS00070; KRINGLE_2; 4.			



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RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchan J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073334; AAH73334.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN AP; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS0070; KRINGLE_2; 4.
DR PROSITE; PS00948; PAN; 1.
DR Kringle.
SQ SEQUENCE 449 AA; 52467 MW; 5C2CE4B708E13D0B CRC64;

Query Match 46.7%; Score 1204.5; DB 2; Length 449;
Best Local Similarity 47.0%; Pred. No. 6.7e-83;
Matches 205; Conservative 74; Mismatches 144; Indels 13; Gaps 6;

OY 5 RNTIEFFKSAKTTLIKIDPALKIKTKKYNVTAADOCANRCTRNKGLPFTCKAFVFDKARQ 64
DB 21 RALNDYQSKGLIELVHMNG-GVKOEIQSEIQVCAKQCS-LLDCRSFYVMKSGS 75

OY 65 CLMFPPNSSGVKKFEGHEFDLYENKDYIRNCTIGKRSYKTVSITSGIKQCPWSSM 124
DB 65 CLMFPPNSSGVKKFEGHEFDLYENKDYIRNCTIGKRSYKTVSITSGIKQCPWSSM 124
DB 76 CHLLPWTQNSANVLLQRNVQYDLYQKDYIRDCVANGNTYRGTVSKTSKGRFCORMLK 135

OY 125 IPHEHY--RGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVECMTCNGE 181
DB 136 FPHDHKFSPIHWPDELEENYCRNPDSPGEGWCYTTDKNIRHQYCGIKKCEDAVCLTCNGE 195

OY 182 SYRGMLDHTESGKICQRMWDQTPHRRKFLPERYPDKGFDNDYCRNPDGQPRPWCYTLDPH 241
DB 196 DYRGSDVDTRESGECQRMWDLQTPHAHPYKREKYPDKSLDNDYCRNPDSSERPMWCYTTDPN 255

OY 242 TRNEYCAITCADNTANDTDVPLETTECTIOGSGEGYRGVNTIANGIPQCRMDSQYPRHH 301
DB 256 VEKEFRITKCKKORSNIEI--TSTCFERGEYRGKANTTSGIPQCRMDSQYPRHH 312

OY 302 DMTPEMFKCKDLAENYCRNPDGSESPMCFSTNDINIVGCSQIPNC-DMSHGQDCYRGNG 360
DB 313 RLPEKYPCKGIDENYCRNPDGSEAPWCFTTLPGMMAVCFQIKRCKDVLLEPDCYHGNG 372

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OY 361 KNVGNLSQTRSGLTCSGMWDMKMDLHRRHIFWEPDASKLKNENYCRNPDDAHGPWCYTCN 420
DB 373 ELYGKRVSKTKRGKRCRMEKREKNDLESLD-QYLVPLEENYCRNPDROSHGWCYTM 431

OY 421 PLIPWDYCPISRCRGG 436
DB 432 PNTPEYDCAIKPCEGE 447

RESULT 12
OY1691 PRELIMINARY; PRT; 716 AA.
AC OY1691;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Growth factor Liverline.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruiz I Alcaba A., Thery C.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U57455; AAB52574.1; -.
DR HSP; P00746; IFDP.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001152; HGF_MST1; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; TRYD_SPE; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS0070; KRINGLE_2; 4.
DR PROSITE; PS00948; PAN; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 716 AA; 81971 MW; 508376A0E4398798 CRC64;

Query Match 46.5%; Score 1198.5; DB 2; Length 716;
Best Local Similarity 46.5%; Pred. No. 3.2e-82;
Matches 205; Conservative 75; Mismatches 148; Indels 13; Gaps 6;

OY 5 RNTIEFFKSAKTTLIKIDPALKIKTKKYNVTAADOCANRCTRNKGLPFTCKAFVFDKARQ 64
DB 31 RALNDYQSKGLIELVHMNG-GVKOEIQSEIQVCAKQCS-LLDCRSFYVMKSGT 85

OY 65 CLMFPPNSSGVKKFEGHEFDLYENKDYIRNCTIGKRSYKTVSITSGIKQCPWSSM 124
DB 86 CHLLPWTQNSANVLLQRNVQYDLYQKDYIRDCVANGNTYRGTVSKTSKGRFCORMLK 145

OY 125 IPHEHY--RGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVECMTCNGE 181
DB 146 FPHDHKFSPIHWPDELEENYCRNPDSPGEGWCYTTDKNIRHQYCGIKKCEDAVCLTCNGE 205

OY 182 SYRGMLDHTESGKICQRMWDQTPHRRKFLPERYPDKGFDNDYCRNPDGQPRPWCYTLDPH 241
DB 206 DYRGSDVDTRESGECQRMWDLQTPHAHPYKREKYPDKSLDNDYCRNPDSSERPMWCYTTDPN 265

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QY 242 TRREYCAIKTCADNTMNDTVPLETTBCTIOGQEGYRGVNTIWMGIPCCQRMDSQYPRHH 301
DB 266 VEKEFRITRITCKKQKORLSNIEI---TSTCFKEREGERGKANTTSGIPCCQRMDSQYPRHH 322
QY 302 DMTPENFKCDLRENYCRNPDGSESPMCFPTTDNINIVGYSQIPNC-DMSHGDDCYRNG 360
DB 323 RLPEKRYPCGDLRENYCRNPDGSESPMCFPTTDNINIVGYSQIPNC-DMSHGDDCYRNG 382
QY 361 KNYMGNLSQTSRGLTCSMDKMDLHRHIFMEPDASKLNENYCRNPDGDAHGPCYTCGN 420
DB 383 ELYSGAVSKTRKIKCRMRKEKNDLESLD-QPIVLEBENYCRNPDGSHGPCYTCMD 441
QY 421 PLIPWDYCPISRCGDTPTTI 441
DB 442 PNTFPDYCAIKPCGEKVLTL 462

RESULT 13
QY 090865 PRELIMINARY; PRT; 704 AA.
AC Q90865;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hepatocyte growth factor-like/macrophage stimulating protein.
GN Name=HGFL/MSP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RX RX SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96029010; PubMed=7554499;
RA Thery C., Sharpe M.J., Bactley S.J., Stern C.D., Gherardi E.;
RT "Expression of HGF/SF, HGFL/MSP and c-met suggests new functions
RT during early chick development.";
RT Dev. Genet. 17:90-101(1995).
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; X84043; CAA58862.1; -.
DR HSP; P00747; ICEA.
DR MEROPS; S01.977; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001152; HGF MST1; 1.
DR PRINTS; PR00723; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; TRYD SP; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS00070; KRINGLE_2; 4.
DR PROSITE; PS00948; PAN; 1.
DR PROSITE; PS02040; TRYPSIN DOM; 1.
DR Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 704 AA; 79341 MW; CAB0D8CC41367C37 CRC64;

Query Match 45.9%; Score 1184; DB 2; Length 704;
Best Local Similarity 45.1%; Pred. No. 3.9e-81;
Matches 202; Conservative 72; Mismatches 150; Indels 24; Gaps 8;

QY 5 RNTIHEFKSATTLLIKIDPALKIKTKKVVATADQANRCSTRNGKLPFTCAVFDKARKO 64
DB 20 RSLNDFQRLRGLELAAAPRPPSPAPAHGAQCCQRCANRP---DCRAFHHEKQSO 75
QY 65 CLWFPNMSGGVKEFGHEFDLYENKDYIRNCIIGKGRSYKQTVSITRSGIKQCPWSM 124

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DB 76 COLLPMSQSPARLQKNHIDLYOKKQFLRECIYANGTSYRGDTRTERGRLCOHWQAT 135
QY 125 IPHESY---RGKDLQENYCRNPDGSESPMCFPTTDNINIVGYSQIPNC-DMSHGDDCYRNG 181
DB 136 TPDHDFPLSLNGBENYCRNPDGSESPMCFPTTDNINIVGYSQIPNC-DMSHGDDCYRNG 195
QY 182 SYRGLMDHTESGKICQRMWDQTPHHKFLPERYPDKGFPDNYCRNPDGQPRPWCYTLDH 241
DB 196 DYRGVFDHTESGTEQQRMDLQHPHGRYPHDXPEKGLDDNYCRNPDGSESPMCFPTTDH 255
QY 242 TRREYCAIKTCADNTMNDTVPLE-TTBTCTIOGQEGYRGVNTIWMGIPCCQRMDSQYPRHH 300
DB 256 LREFFCIRIVCKKRRP-----PINVTGCGYRGKGEYGRVAVTVSGIPCCQRMWDQTLHR 310
QY 301 DMTPENFKCDLRENYCRNPDGSESPMCFPTTDNINIVGYSQIPNC-DMSHGDDCYRNG 359
DB 311 HHFVDSKTPCKDLQENYCRNPDGSESPMCFPTTDNINIVGYSQIPNC-DMSHGDDCYRNG 370
QY 360 GKNYMGNLSQTSRGLTCSMDKMDLHRHIFMEPDASKLNENYCRNPDGDAHGPCYTCGN 414
DB 371 GERYHGVSKTRKIKCRMRKEKNDLESLD-QPIVLEBENYCRNPDGSHGPCYTCMD 425
QY 415 WCYTGNDPLIPWDYCPISRCGDTPTTI 442
DB 426 WCYTGNDPLIPWDYCPISRCGDTPTTI 453

RESULT 14
HGFL HUMAN
ID HGFL_HUMAN STANDARD; PRT; 711 AA.
AC P26927; Q13350; Q14870;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hepatocyte growth factor-like protein precursor (Macrophage
DE stimulatory protein) (MSP) (Macrophage stimulating protein).
GN Name=MST1; Synonyms=HGFL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RX RX SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92002016; PubMed=1655021;
RA Han S., Stuart L.A., Fritzen Degen S.J.;
RT "Characterization of the DNF152 locus on human chromosome 3:
RT identification of a gene coding for four kringle domains with homology
RT to hepatocyte growth factor.";
RT Biochemistry 30:9768-9780(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93340141; PubMed=8393443;
RA Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;
RT "Cloning, sequencing, and expression of human macrophage stimulating
RT protein (MSP, MST1) confirms MSP as a member of the family of kringle
RT proteins and locates the MSP gene on chromosome 3.";
RT J. Biol. Chem. 268:15461-15468(1993).
RN [3]
RP SEQUENCE OF 230-247; 288-310; 326-341; 484-501; 530-549; 574-596 AND
RP 602-611, AND SUBUNIT.
RC TISSUE=Plasma;
RX PubMed=1827141;
RA Skeel A., Yoshimura T., Showalter S.D., Tanaka S., Appella E.,
RA Leonard E.J.;
RT "Macrophage stimulating protein: purification, partial amino acid
RT sequence, and cellular activity.";
RT J. Exp. Med. 173:1227-1234(1991).
CC -1- FUNCTION: Probably has no proteolytic activity, since crucial AA
CC characteristic of serine proteases catalytic sites are not
CC conserved.

```



CC -1- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a  
 CC disulfide bond.  
 CC -1- PTM: May be cleaved after Arg-483, to yield two chains held  
 CC together by disulfide bonds, or two separate polypeptides.  
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 1 kringle domains.  
 CC -1- SIMILARITY: Contains 1 PAN domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL, M74178; AAA50165.1; -  
 CC EMBL, U37055; AAC50471.1; -  
 CC EMBL, L11924; AAA59872.1; -  
 CC PIR, A40331; A47136.  
 CC HSSP, P00766; 1CHG.  
 CC MEROPS, S01.975; -  
 CC Genew, HGNC:7380; MST1.  
 CC MIM, 142408; -  
 CC InterPro: IPR000001; Kringle.  
 CC InterPro: IPR003014; PAN.  
 CC InterPro: IPR003609; Pan app.  
 CC InterPro: IPR009003; Pept\_Ser\_Cys.  
 CC InterPro: IPR001254; Peptidase\_S1.  
 CC InterPro: IPR001314; Peptidase\_S1A.  
 CC InterPro: IPR003966; Peptidase\_S1A\_pr.  
 CC Pfam, PF00051; Kringle; 4.  
 CC Pfam, PF00024; PAN; 1.  
 CC Pfam, PF00089; Trypsin; 1.  
 CC PIRSF, PIRSF001152; HGF\_MST1; 1.  
 CC PRINTS, PR00722; CHYMOTRYPSIN.  
 CC PRINTS, PR00018; KRINGLE.  
 CC PRODOM, PDO00395; Kringle; 4.  
 CC SMART, SM00130; KR; 4.  
 CC SMART, SM00473; PAN\_AP; 1.  
 CC SMART, SM00020; TRY\_P\_SPC; 1.  
 CC PROSITE, PS00021; KRINGLE\_1; 4.  
 CC PROSITE, PS00070; KRINGLE\_2; 4.  
 CC PROSITE, PS50948; PAN; 1.  
 CC PROSITE, PS50240; TRYPSIN\_DOM; 1.  
 CC Direct protein sequencing; Glycoprotein; Kringle; Polymorphism;  
 CC Repeat; Serine protease homolog; Signal.  
 CC SIGNAL, 18  
 CC CHAIN, 19  
 CC DOMAIN, 21  
 CC DOMAIN, 110  
 CC DOMAIN, 191  
 CC DOMAIN, 283  
 CC DOMAIN, 370  
 CC DOMAIN, 484  
 CC DOMAIN, 56  
 CC DISULFID, 60  
 CC DISULFID, 110  
 CC DISULFID, 131  
 CC DISULFID, 157  
 CC DISULFID, 181  
 CC DISULFID, 194  
 CC DISULFID, 212  
 CC DISULFID, 240  
 CC DISULFID, 283  
 CC DISULFID, 304  
 CC DISULFID, 332  
 CC DISULFID, 370  
 CC DISULFID, 391  
 CC DISULFID, 419  
 CC DISULFID, 468

FT DISULFID 507 523 By similarity.  
 FT DISULFID 602 667 By similarity.  
 FT DISULFID 632 646 By similarity.  
 FT DISULFID 657 685 By similarity.  
 FT CARBOHYD 72 72 N-linked [GlcNAc. . .] (Potential).  
 FT CARBOHYD 296 296 N-linked [GlcNAc. . .] (Potential).  
 FT CARBOHYD 615 615 N-linked [GlcNAc. . .] (Potential).  
 FT VARIANT 13 13 Y -> C.  
 FT VARIANT 212 212 C -> F.  
 FT VARIANT 676 676 E -> K (in dbSNP:7798).  
 FT CONFLICT 292 292 R -> G (in Ref. 3).  
 FT CONFLICT 304 304 C -> E (in Ref. 3).  
 FT CONFLICT 306 306 R -> E (in Ref. 3).  
 FT CONFLICT 550 551 PS -> SL (in Ref. 3).  
 FT CONFLICT 593 593 W -> E (in Ref. 3).  
 FT CONFLICT 623 623 L -> F (in Ref. 2).  
 SQ SEQUENCE 711 AA; 80379 MW; 596ED21F180290E4 CRC64;  
 Query Match 45.4%; Score 1171; DB 1; Length 711;  
 Best Local Similarity 47.3%; Pred. No. 3.8e-80;  
 Matches 196; Conservative 60; Mismatches 148; Indels 10; Gaps 4;  
 QY 33 VNTADQCANRCTRKNKGLPFTCKAFVFDKARQCLMPFNSNSGVKKEFGHEPDLYENKD 92  
 DB 50 VADAECCAGRC---GPLMDGRAFHVYNSHGCOLLPWTOHSPHTRLRSGRCDLFOKXD 105  
 QY 93 YIRNCIIKKGKSYGKTSYTSYGKICQDPMSMITHESYR---GKLDQENCRNPRGEG 149  
 DB 106 YVRCITMNNGVGYGTATVTVGGLPCQAMSHKFPNDHYRTTLRNGEENCRNPDGPG 165  
 QY 150 GPMCFPTSNPEVRYEVCDDPOCEVECMTCNGESRYGLMDHTESGKICQRMHQPRIHKEF 209  
 DB 166 GPMCTTDPNPAVRFQSGCGIKSCREACVWCNEEYRGAVDRTESGECQRMQLQHPHQPF 225  
 QY 210 LPERYPDKGPDNCRNPDGQPRPWCYTLDPHTWREYCAIKTCADNTMNDTVPLETTEC 269  
 DB 226 EPGKFLDGLDDNVCNPDGSEIRPWCYTDDQIREFCDLPRCSEAPROEA--TVSC 283  
 QY 270 IQGGESEGRGVNTIMNGICPQQRWDSQYPRHDMTPENFKCDLRNCRNPDGSESPWC 329  
 DB 284 FRKGESEGRGVNTTAVPQQRWDAQIPHQHFRFPPEYACKDKRENCRNPDGSEAPWC 343  
 QY 330 FTTDPNIVGVCSQIPNC-DMSHGDCYRGKNGKMYGNTLSQTRSGLTCSMDKXMEDLAR 388  
 DB 344 FTLRGMRAAFCYQIRRCTDVRPDQCYHGAQEYRGVSKTRKGVOCQKSAETPHKQ 403  
 QY 389 HIFWEPDASKLNENCRNPDGDAHGPWCYTGNPLIPWDYCPISRCGDTPTTV 442  
 DB 404 FTFTEPHQAQLEENCRNPDGDSHPWCYTMDPRTPFYCALRRCADQPPSIL 457  
 RESULT 15  
 ID P70006 PRELIMINARY; PRT; 717 AA.  
 AC P70006: 01-FEB-1997 (Tremblrel. 02, Created)  
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Hepatocyte growth factor-like protein precursor.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NCBI\_TaxID=8355;  
 RN NCB1  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney, and Liver;  
 RX MEDLINE=96404125; PubMed=8808403; DOI=10.1016/0925-4773(95)00458-0;  
 RA Aberger F., Schmidt G., Richter K.;  
 RT "The Xenopus genome of hepatocyte growth factor-like protein is





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OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:29 ; Search time 170.535 seconds  
(without alignments)  
1002.420 Million cell updates/sec

Title: US-09-674-377B-2

Perfect score: 2579  
Sequence: 1 ERKRNTHIEFKSAKTLTI.....IPWDYCPISRCBGDTPTIV 442

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp19808:\*  
2: geneseqp19908:\*  
3: geneseqp20008:\*  
4: geneseqp20015:\*  
5: geneseqp20025:\*  
6: geneseqp20035:\*  
7: geneseqp20035:\*  
8: geneseqp20045:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2576	99.9	442	7	ADM83267 Human NK4
2	2576	99.9	723	2	AAR07144 Tumour cy
3	2576	99.9	723	2	AAR15624 Human leu
4	2576	99.9	723	2	AAR15624 Human leu
5	2576	99.9	723	2	AAR57027 Recombina
6	2576	99.9	723	2	AAR57028 Human mod
7	2576	99.9	723	2	AAR57026 Human wil
8	2576	99.9	723	2	AAR82685 Tumour cy
9	2576	99.9	723	2	AAR76690 Human pla
10	2576	99.9	723	2	AAY06621 HGF-MSP h
11	2576	99.9	723	2	AAY06622 HGF-MSP h
12	2576	99.9	1109	7	ADDB9672 ChimERIC
13	2574	99.8	442	3	AAY57174 N-termina
14	2573	99.8	723	2	AAR21142 Human TCF
15	2566	99.5	723	2	AAM59923 Human leu
16	2565	99.5	504	2	AAR32710 Haematopo
17	2563.5	99.4	447	7	ADB37393 Human hep
18	2563.5	99.4	447	7	ADM83266 Human NK4
19	2563.5	99.4	697	3	AAY8485 Hepatocyt
20	2563.5	99.4	697	3	AAY59030 Sequence
21	2563.5	99.4	697	4	AAB45838 Nucleic a
22	2563.5	99.4	697	4	AAB45838 Nucleic a
23	2563.5	99.4	728	2	AAR25676 Recombina
24	2563.5	99.4	728	2	AAR20005 Human hep
25	2563.5	99.4	728	2	AAR40862 Competati

26	2563.5	99.4	728	2	AAR40863 Competati
27	2563.5	99.4	728	2	AAR42062 Vascular
28	2563.5	99.4	728	2	AAR87522 Mutant he
29	2563.5	99.4	728	2	AAR87524 Mutant he
30	2563.5	99.4	728	2	AAR87525 Mutant he
31	2563.5	99.4	728	2	AAR87523 Mutant he
32	2563.5	99.4	728	2	AAM00340 Wild type
33	2563.5	99.4	728	2	AAM00338 Human hep
34	2563.5	99.4	728	2	AAM59922 Human leu
35	2563.5	99.4	728	2	AAM58696 Human hep
36	2563.5	99.4	728	2	AAM42998 Recombina
37	2563.5	99.4	728	2	AAM39207 Human hep
38	2563.5	99.4	728	6	ABP58128 Human hep
39	2563.5	99.4	728	7	ADB61534 Hepatocyt
40	2563.5	99.4	728	8	ADM97652 Human hep
41	2563.5	99.4	728	8	ADR89322 Human hep
42	2563.5	99.4	951	8	ADS19044 ChimERIC
43	2561.5	99.3	447	3	AAY57173 N-termina
44	2557.5	99.2	727	2	AAR10656 Hepatic p
45	2557.5	99.2	728	2	AAR15623 Human leu

# ALIGNMENTS

RESULT 1	ADM83267	ADM83267 standard; protein; 442 AA.
XX	AC	ADM83267;
XX	DT	18-NOV-2004 (first entry)
XX	XX	Human NK4 protein #2.
DE	XX	
XX	KW	NK4 gene; neovascularisation; ovarian cancer; pancreatic cancer;
XX	KW	stomach cancer; gallbladder cancer; renal cancer; prostatic cancer;
XX	KW	breast cancer; esophageal cancer; hepatic cancer; oral cavity cancer;
XX	KW	colon cancer; colorectal cancer; sarcoma; glioma; melanoma; gene therapy;
XX	OS	human.
XX	OS	Homo sapiens.
XX	PN	US2003162736-A1.
XX	PN	26-AUG-2003.
XX	PD	27-SEP-2002; 2002US-00255649.
XX	PF	25-FEB-2002; 2002JP-0048644.
XX	PR	(NARA/) NAKAMURA T.
PA	PA	(MATS/) MATSUMOTO K.
PI	PI	Nakamura T, Matsumoto K;
XX	DR	WPI: 2003-897946/82.
XX	DR	N-PSDB; ADM83265.
XX	PT	New NK4 gene, useful for producing a medicament for preventing or
XX	PT	treating diseases caused by neovascularization, e.g. cancer.
XX	PS	Disclosure; Page 17-19; 27pp; English.
CC	CC	The present invention provides a therapeutic agent NK4 polypeptides and
CC	CC	their encoding polynucleotides. The invention is useful for producing a
CC	CC	medicament for preventing or treating diseases caused by
CC	CC	neovascularisation such as ovarian cancer, pancreatic cancer, stomach
CC	CC	cancer, gallbladder cancer, renal cancer, prostatic cancer, breast
CC	CC	cancer, esophageal cancer, hepatic cancer, oral cavity cancer, colon
CC	CC	cancer, colorectal cancer, sarcoma, glioma and melanoma. The invention is
XX	XX	also useful in gene therapy. The present sequence is human NK4 protein.

SQ Sequence 442 AA;

Query Match 99.9%; Score 2576; DB 7; Length 442;  
 Best Local Similarity 99.8%; Pred. No. 8.5e-164;  
 Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRRNTIHEFKSAKTTLLIKIDPALKIKTKKVTADOCANRCTRNKGLPFTCAAFVFDK 60  
 DB 1 ORKRRNTIHEFKSAKTTLLIKIDPALKIKTKKVTADOCANRCTRNKGLPFTCAAFVFDK 60  
 QY 61 ARKOCLEPPFNSMSGVKKERGFHEFDLYENKDYINNCIIGKRSYKGVSTITKSGIKOP 120  
 DB 61 ARKOCLEPPFNSMSGVKKERGFHEFDLYENKDYINNCIIGKRSYKGVSTITKSGIKOP 120  
 QY 121 WSSMIPHEHSYRGKDLQENYCRNPRGEGGFWCTSNPEVREYVCDIPQSEVECMTCNG 180  
 DB 121 WSSMIPHEHSYRGKDLQENYCRNPRGEGGFWCTSNPEVREYVCDIPQSEVECMTCNG 180  
 QY 181 ESYRGLMDHTESGKICQRMHQTPHRAKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240  
 DB 181 ESYRGLMDHTESGKICQRMHQTPHRAKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240  
 QY 241 HTRWEYCAIKTCADNTMDTVPLETTETCIGQSGEGYRGVTNTIWNIGIPCORMBSQYPHE 300  
 DB 241 HTRWEYCAIKTCADNTMDTVPLETTETCIGQSGEGYRGVTNTIWNIGIPCORMBSQYPHE 300  
 QY 301 HDMPENFKCKDLRENYCRNPDGSESFWCTTDNIRVGYCSQIPNCDSHGDQCYRGNG 360  
 DB 301 HDMPENFKCKDLRENYCRNPDGSESFWCTTDNIRVGYCSQIPNCDSHGDQCYRGNG 360  
 QY 361 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 420  
 DB 361 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 420  
 QY 421 PLIPWDYCPISRCBGDTTPTIV 442  
 DB 421 PLIPWDYCPISRCBGDTTPTIV 442

RESULT 2

AAR07144 standard; protein; 723 AA.

AC AAR07144;  
 XX  
 AC AAR07144;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 31-JAN-1991 (first entry)  
 XX  
 DE Tumour cytotoxic factor II.  
 XX  
 KW TCF II; glycoprotein; fibroblasts; anticancer agent.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..29  
 XX  
 EN WO9010651-A.  
 XX  
 PD 20-SEP-1990.  
 XX  
 PF 10-MAR-1989; 89JP-00058631.  
 XX  
 PR 10-MAR-1989; 89JP-00058631.  
 PR 16-JAN-1990; 90JP-00006692.  
 XX  
 PA (SNOW ) SNOW BRAND MILK PROD CO LTD.  
 XX  
 PI Higashio K, Mitsuda S, Shima N, Itagaki Y, Nagao M,  
 XX  
 DR WPI; 1990-304990/40.  
 DR P-PSDB; AAR07144.  
 XX

PT Human glyco:protein having antitumour activity - for inducing  
 PT differentiation of leukaemia cells and enhancing cell mediated immunity.  
 XX  
 PS Disclosure; Fig 15; 73pp; Japanese.

CC The sequence was deduced from the cDNA obtd. from a clone isolated from a  
 CC cDNA library prepd. from RNA extd. from fibroblast IMR-90 cells (ATCC CCL  
 CC -186). The N-terminal of the alpha chain is unclear. The sequence shows  
 CC homology to hGF except between AAs 162 and 166 of this sequence which is  
 CC absent from the TCF-II sequence. The DNA can be used to produce the TCF  
 CC II by recombinant DNA technology. TCF II is an anticancer agent and  
 CC induces differentiation of leukaemia cells, enhances cell-mediated  
 CC immunity, and accelerates the proliferation of human blood vessel  
 CC endothelial cells and hepatic parenchymal cells. (updated on 25-MAR-2003  
 CC to correct PR field.) (updated on 25-MAR-2003 to correct PA field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX

SQ Sequence 723 AA;

Query Match 99.9%; Score 2576; DB 2; Length 723;  
 Best Local Similarity 99.8%; Pred. No. 1.4e-163;  
 Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRRNTIHEFKSAKTTLLIKIDPALKIKTKKVTADOCANRCTRNKGLPFTCAAFVFDK 60  
 DB 32 ORKRRNTIHEFKSAKTTLLIKIDPALKIKTKKVTADOCANRCTRNKGLPFTCAAFVFDK 91  
 QY 61 ARKOCLEPPFNSMSGVKKERGFHEFDLYENKDYINNCIIGKRSYKGVSTITKSGIKOP 120  
 DB 92 ARKOCLEPPFNSMSGVKKERGFHEFDLYENKDYINNCIIGKRSYKGVSTITKSGIKOP 151  
 QY 121 WSSMIPHEHSYRGKDLQENYCRNPRGEGGFWCTSNPEVREYVCDIPQSEVECMTCNG 180  
 DB 152 WSSMIPHEHSYRGKDLQENYCRNPRGEGGFWCTSNPEVREYVCDIPQSEVECMTCNG 211  
 QY 181 ESYRGLMDHTESGKICQRMHQTPHRAKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240  
 DB 212 ESYRGLMDHTESGKICQRMHQTPHRAKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271  
 QY 241 HTRWEYCAIKTCADNTMDTVPLETTETCIGQSGEGYRGVTNTIWNIGIPCORMBSQYPHE 300  
 DB 272 HTRWEYCAIKTCADNTMDTVPLETTETCIGQSGEGYRGVTNTIWNIGIPCORMBSQYPHE 331  
 QY 301 HDMPENFKCKDLRENYCRNPDGSESFWCTTDNIRVGYCSQIPNCDSHGDQCYRGNG 360  
 DB 332 HDMPENFKCKDLRENYCRNPDGSESFWCTTDNIRVGYCSQIPNCDSHGDQCYRGNG 391  
 QY 361 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 420  
 DB 392 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 451  
 QY 421 PLIPWDYCPISRCBGDTTPTIV 442  
 DB 452 PLIPWDYCPISRCBGDTTPTIV 473

RESULT 3

AAR15624 standard; protein; 723 AA.

AC AAR15624;  
 XX  
 AC AAR15624;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 18-MAR-1992 (first entry)  
 XX  
 DE Human leukocyte-derived HGF encoded by clone HLC3.  
 XX  
 KW Hepatocyte growth factor; liver; hepatoma.  
 XX  
 OS Homo sapiens.  
 XX  
 DR EP461560-A.  
 XX

PD 18-DEC-1991.  
XX  
PF 07-JUN-1991; 91EP-00109369.  
XX  
PR 11-JUN-1990; 90JP-00152474.  
XX  
PA (TOYM ) TOYO BOSEKI KK.  
XX  
PI Nakamura T, Hagiya M, Seki T, Shimomishi M, Shimizu S, Ihara I;  
PI Sakauchi M, Asami O;  
XX  
DR WPI: 1991-370578/51.  
DR N-PSDB; AAQ15177.  
XX  
PT Recombinant human leukocyte-derived hepatocyte growth factor - with DNA  
PT encoding it, recombinant expression vectors and transformant cells  
PT expressing it.  
XX  
PS Claim 3; Fig 3; 33pp; English.  
XX  
CC The sequence was deduced from a portion of HUC3, one of two clones, (for  
CC HUC2 see AAR15623) isolated from a cDNA library prepd. from mRNA  
CC extracted from human leukocytes. HUC2 has almost the same sequence as  
CC HUC3 except for five residues (162-166) in HUC2 which do not appear in  
CC HUC3. HUC3 shows similar characteristics to the human liver-derived HGF  
CC identified in Nature, 342, 440, 1989, but differs at 14 positions in the  
CC amino acid sequence. The DNA sequence can be expressed and the resulting  
CC protein, recombinant HGF, used in hepa- tocyte cultivation, liver  
CC regeneration, hepatocyte research, esp. into the mechanism of hepatoma,  
CC and to prepare anti-HGF antibodies for diagnosis and therapy. (Updated on  
CC 25-MAR-2003 to correct PI field.)  
XX  
XX  
SQ Sequence 723 AA;  
XX  
Query Match 99.9%; Score 2576; DB 2; Length 723;  
Best Local Similarity 99.8%; Pred. No. 1.4e-163;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ERKRRNTIHEFKSAKTLTIKIDPALKITKVNNTADOCANRCTRNKGLPFTCKAFVFDK 60  
DB :|||||  
32 QKRRNTIHEFKSAKTLTIKIDPALKITKVNNTADOCANRCTRNKGLPFTCKAFVFDK 91  
QY 61 ARKQCLMPFPNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKCP 120  
DB 92 ARKQCLMPFPNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKCP 151  
QY 121 WSMIPIHSHSYRGKDLQENYCRNPRGEGGPMCFNSPEVRYEVDIQCSEVECMTCNG 180  
DB 152 WSMIPIHSHSYRGKDLQENYCRNPRGEGGPMCFNSPEVRYEVDIQCSEVECMTCNG 211  
QY 181 ESYRGLMDHTESGKICQRMWDHQTPIRHAKFLPERYPDKGFDDNYCRNPDGQRPWCYTLDP 240  
DB 212 ESYRGLMDHTESGKICQRMWDHQTPIRHAKFLPERYPDKGFDDNYCRNPDGQRPWCYTLDP 271  
QY 241 HTRWEYCAIKTCADNTMNDTVPLETTTECIGQGEGYRGTVNTIWNIGIPCORWDSQYPHE 300  
DB 272 HTRWEYCAIKTCADNTMNDTVPLETTTECIGQGEGYRGTVNTIWNIGIPCORWDSQYPHE 331  
QY 301 HDMTPENFKCDLRNRYCRNPDGSSPWCFTTDPNIRVGYCSQIPNCMSHGQDCYRNG 360  
DB 332 HDMTPENFKCDLRNRYCRNPDGSSPWCFTTDPNIRVGYCSQIPNCMSHGQDCYRNG 391  
QY 361 KNYMGNLSQTRSGLTCSMDKNMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPWCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMDKNMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPWCYTGN 451  
QY 421 PLIPWDYCPISRCBGDTTPTIV 442  
DB 452 PLIPWDYCPISRCBGDTTPTIV 473  
RESULT 4  
AAR25677

ID AAR25677 standard; protein; 723 AA.  
XX  
XX AAR25677;  
AC  
XX  
XX 20-JUN-1993 (first entry)  
XX  
XX Recombinant human hepatocyte growth factor.  
DE  
XX HGF; enhance growth; preparing transgenic animals; hepatic disease;  
KW clinical diagnostic reagent; drug.  
XX  
XX Homo sapiens.  
XX  
XX JP04183394-A.  
PN  
XX  
PD 30-JUN-1992.  
XX  
PF 19-NOV-1990; 90JP-00314548.  
XX  
XX 19-NOV-1990; 90JP-00314548.  
PR 19-NOV-1990; 90JP-00314548.  
XX  
XX (TOYM ) TOYOBO KK.  
PA (NAKA/) NAKAMURA T.  
XX  
DR WPI: 1992-265591/32.  
XX  
XX Recombinant human hepatocyte growth factor and DNA encoding it - useful  
PT for diagnosis and treatment of hepatic disease and transgenic animal  
PT prepn.  
XX  
XX Disclosure; Page 13; 28pp; Japanese.  
XX  
XX  
XX This sequence represents a recombinant human hepatocyte growth factor. It  
CC has physiological activity, and using it enhanced growth of hepatocytes  
CC is possible. It is useful as a clinical diagnostic reagent, or a drug for  
CC treating hepatic disease. See also AAR25676-92, AAQ26713-27  
XX  
XX  
SQ Sequence 723 AA;  
XX  
Query Match 99.9%; Score 2576; DB 2; Length 723;  
Best Local Similarity 99.8%; Pred. No. 1.4e-163;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ERKRRNTIHEFKSAKTLTIKIDPALKITKVNNTADOCANRCTRNKGLPFTCKAFVFDK 60  
DB :|||||  
32 QKRRNTIHEFKSAKTLTIKIDPALKITKVNNTADOCANRCTRNKGLPFTCKAFVFDK 91  
QY 61 ARKQCLMPFPNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKCP 120  
DB 92 ARKQCLMPFPNSMSGVKKFEGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKCP 151  
QY 121 WSMIPIHSHSYRGKDLQENYCRNPRGEGGPMCFNSPEVRYEVDIQCSEVECMTCNG 180  
DB 152 WSMIPIHSHSYRGKDLQENYCRNPRGEGGPMCFNSPEVRYEVDIQCSEVECMTCNG 211  
QY 181 ESYRGLMDHTESGKICQRMWDHQTPIRHAKFLPERYPDKGFDDNYCRNPDGQRPWCYTLDP 240  
DB 212 ESYRGLMDHTESGKICQRMWDHQTPIRHAKFLPERYPDKGFDDNYCRNPDGQRPWCYTLDP 271  
QY 241 HTRWEYCAIKTCADNTMNDTVPLETTTECIGQGEGYRGTVNTIWNIGIPCORWDSQYPHE 300  
DB 272 HTRWEYCAIKTCADNTMNDTVPLETTTECIGQGEGYRGTVNTIWNIGIPCORWDSQYPHE 331  
QY 301 HDMTPENFKCDLRNRYCRNPDGSSPWCFTTDPNIRVGYCSQIPNCMSHGQDCYRNG 360  
DB 332 HDMTPENFKCDLRNRYCRNPDGSSPWCFTTDPNIRVGYCSQIPNCMSHGQDCYRNG 391  
QY 361 KNYMGNLSQTRSGLTCSMDKNMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPWCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMDKNMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPWCYTGN 451  
QY 421 PLIPWDYCPISRCBGDTTPTIV 442  
DB 452 PLIPWDYCPISRCBGDTTPTIV 473

Db 452 PLIPWDYCPISRCBGDTTPTIV 473

RESULT 5  
AAR57027  
ID AAR57027 standard; protein; 723 AA.  
XX  
XX AAR57027;  
AC  
XX 25-MAR-2003 (revised)  
DT 19-MAR-1995 (first entry)  
XX  
XX Human modified tumor cytotoxic factor.  
DE  
XX Tumor cytotoxic factor; hepatocyte growth factor; antitumor.  
XX  
XX Homo sapiens.  
OS  
XX MO9414845-A1.  
PN  
XX 07-JUL-1994.  
PD  
XX 27-DEC-1993; 93WO-JP001905.  
PF  
XX 28-DEC-1992; 92JP-00359747.  
PR  
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.  
PA  
XX Yamaguchi K, Shima N, Murakami A, Goto M, Tsuda E, Masunaga H;  
PI Takahira R, Oogaki F, Ueda M, Higashio K;  
XX WPI; 1994-234619/28.  
DR  
XX Modified tumour cytotoxic factors with loss of binding of N-linked  
PT oligosaccharide chain - have longer biological half-life without loss of  
PT biological activity.  
XX  
XX Claim 5; Page 33; 59pp; English.  
PS  
XX This modified TCF sequence has a prolonged biological half-life without  
CC any loss of biological activity, is obtained by altering the amino acid  
CC residue at position 563 from Ser in the wild-type to Ala. (Updated on 25-  
CC MAR-2003 to correct PN field.)  
XX  
XX Sequence 723 AA;  
SQ

Query Match 99.9%; Score 2576; DB 2; Length 723;  
Best Local Similarity 99.8%; Pred. No. 1,4e-163;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRRTTHERFKSAKTTLLIKIDPALKIKTKKVNTPADOCANRCTRNKGLPTCKAFVFDK 60  
:|||||  
DB 32 QKRKRTTHERFKSAKTTLLIKIDPALKIKTKKVNTPADOCANRCTRNKGLPTCKAFVFDK 91  
61 ARKQCLMPFPNMSGVKKFGEHFDLYENKDYIRNCIIIGRSYKGVTSITKSGIKQCP 120  
DB 92 ARKQCLMPFPNMSGVKKFGEHFDLYENKDYIRNCIIIGRSYKGVTSITKSGIKQCP 151  
121 WSSMTPHHSYRGKDLQENYCRNPRGEGGFCFTSNPEVRYEVCIDIPOCSEVECMTCNG 180  
DB 152 WSSMTPHHSYRGKDLQENYCRNPRGEGGFCFTSNPEVRYEVCIDIPOCSEVECMTCNG 211  
181 ESYRGLMDHTESGKICQKWDHOTPHRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLDP 240  
DB 212 ESYRGLMDHTESGKICQKWDHOTPHRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLDP 271  
241 HTRWEXCAIKTCADNTMNDTVPLETTBECIOGSEGYRGTIVTWNGIPQCRWDSQYRHE 300  
DB 272 HTRWEXCAIKTCADNTMNDTVPLETTBECIOGSEGYRGTIVTWNGIPQCRWDSQYRHE 331  
301 HMTPEPFCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCMDSHGQDCYRGNG 360  
DB 332 HMTPEPFCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCMDSHGQDCYRGNG 391

QY 361 KNYMGNLSQTRSSGLTCSMDKXNMDLHRHIFWEPDASKLNENYCRNPDDBAHGWCYTG 420  
DB 392 KNYMGNLSQTRSSGLTCSMDKXNMDLHRHIFWEPDASKLNENYCRNPDDBAHGWCYTG 451

QY 421 PLIPWDYCPISRCBGDTTPTIV 442  
:|||||  
DB 452 PLIPWDYCPISRCBGDTTPTIV 473

RESULT 6  
AAR57028  
ID AAR57028 standard; protein; 723 AA.  
XX  
XX AAR57028;  
AC  
XX 25-MAR-2003 (revised)  
DT 19-MAR-1995 (first entry)  
XX  
XX Human modified tumor cytotoxic factor.  
DE  
XX Tumor cytotoxic factor; hepatocyte growth factor; antitumor.  
XX  
XX Homo sapiens.  
OS  
XX MO9414845-A1.  
PN  
XX 07-JUL-1994.  
PD  
XX 27-DEC-1993; 93WO-JP001905.  
PF  
XX 28-DEC-1992; 92JP-00359747.  
PR  
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.  
PA  
XX Yamaguchi K, Shima N, Murakami A, Goto M, Tsuda E, Masunaga H;  
PI Takahira R, Oogaki F, Ueda M, Higashio K;  
XX WPI; 1994-234619/28.  
DR  
XX Modified tumour cytotoxic factors with loss of binding of N-linked  
PT oligosaccharide chain - have longer biological half-life without loss of  
PT biological activity.  
XX  
XX Claim 6; Page 33; 59pp; English.  
PS  
XX This modified TCF sequence has a prolonged biological half-life without  
CC any loss of biological activity, is obtained by altering the amino acid  
CC residue at position 563 from Ser in the wild-type to Ala. (Updated on 25-  
CC MAR-2003 to correct PN field.)  
XX  
XX Sequence 723 AA;  
SQ

Query Match 99.9%; Score 2576; DB 2; Length 723;  
Best Local Similarity 99.8%; Pred. No. 1,4e-163;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRRTTHERFKSAKTTLLIKIDPALKIKTKKVNTPADOCANRCTRNKGLPTCKAFVFDK 60  
:|||||  
DB 32 QKRKRTTHERFKSAKTTLLIKIDPALKIKTKKVNTPADOCANRCTRNKGLPTCKAFVFDK 91  
61 ARKQCLMPFPNMSGVKKFGEHFDLYENKDYIRNCIIIGRSYKGVTSITKSGIKQCP 120  
DB 92 ARKQCLMPFPNMSGVKKFGEHFDLYENKDYIRNCIIIGRSYKGVTSITKSGIKQCP 151  
121 WSSMTPHHSYRGKDLQENYCRNPRGEGGFCFTSNPEVRYEVCIDIPOCSEVECMTCNG 180  
DB 152 WSSMTPHHSYRGKDLQENYCRNPRGEGGFCFTSNPEVRYEVCIDIPOCSEVECMTCNG 211  
181 ESYRGLMDHTESGKICQKWDHOTPHRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLDP 240  
DB 212 ESYRGLMDHTESGKICQKWDHOTPHRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLDP 271

QY 241 HTRMEYCAIKTCADTMDTVDVPLETTECICQGGEGYRGTVNTWNGICPCQWDSQYPHE 300  
DB 272 HTRMEYCAIKTCADTMDTVDVPLETTECICQGGEGYRGTVNTWNGICPCQWDSQYPHE 331  
QY 301 HMTPEPFCKDRLRENYCENPDGSSPWCFTTDPNIRVGCQIIPNCDSHQDCYRANG 360  
DB 332 HMTPEPFCKDRLRENYCENPDGSSPWCFTTDPNIRVGCQIIPNCDSHQDCYRANG 391  
QY 361 KNYMGNLSQTRSGLTCSMDKXMDLHRHIFWEPDASKLENYCRNPDDAHGPWCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMDKXMDLHRHIFWEPDASKLENYCRNPDDAHGPWCYTGN 451  
QY 421 PLIPMDYCPISRCEGDTPTTIV 442  
DB 452 PLIPMDYCPISRCEGDTPTTIV 473

RESULT 7  
AAR57026  
ID AAR57026 standard; protein; 723 AA.  
XX AAR57026;  
AC AAR57026;  
XX  
XX 25-MAR-2003 (revised)  
DT 19-MAR-1995 (first entry)  
XX  
XX Human wild-type tumor cytotoxic factor.  
DE  
XX Tumor cytotoxic factor; hepatocyte growth factor; antitumor.  
KM  
XX Homo sapiens.  
OS  
XX WO9414845-A1.  
XX  
XX 07-JUL-1994.  
XX PD  
XX 27-DEC-1993; 93WO-JP001905.  
PF  
XX 28-DEC-1992; 92JP-00359747.  
PR  
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.  
PA  
XX Yamaguchi K, Shima N, Murakami A, Goto M, Teuda E, Masunaga H;  
PI Takahira R, Oogaki F, Ueda M, Higashio K;  
XX  
XX WPI; 1994-234619/28.  
DR  
XX Modified tumour cytotoxic factors with loss of binding of N-linked  
PT oligosaccharide chain - have longer biological half-life without loss of  
XX biological activity.  
XX  
XX Disclosure; Page 29; 59pp; English.  
XX  
XX This TCF sequence may be modified in that the AA residues responsible for  
CC binding of N-linked oligosaccharide chains are prevented so that at least  
CC one of the N-linked oligosaccharide chains is provided from binding to  
CC TCF. Ser-563 may be substituted with Ala (AAR57027) or Asn-289  
CC substituted with Gln (AAR57028). (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
XX Sequence 723 AA;  
SQ

Query Match 99.9%; Score 2576; DB 2; Length 723;  
Best Local Similarity 99.8%; Pred. No. 1.4e-163;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKKRRNTIHFKKSAKTLIKIDPALKIKTKKVTADQCANCTRNKGLPTCKAFVFDK 60  
DB 32 QKKRRNTIHFKKSAKTLIKIDPALKIKTKKVTADQCANCTRNKGLPTCKAFVFDK 91  
QY 61 ARKQCIWPFPPNSGSSGVKKEFGHEPDLNENKDYIRNCIIGKRSYKGTVSITKSGIKCP 120  
DB 92 ARKQCIWPFPPNSGSSGVKKEFGHEPDLNENKDYIRNCIIGKRSYKGTVSITKSGIKCP 151

QY 121 WSSMI.PHEHSYRGKDLQENYCRNPRGEGGPMCFSTSNPEVRYEVCIDIPOCSEVECTCNG 180  
DB 152 WSSMI.PHEHSYRGKDLQENYCRNPRGEGGPMCFSTSNPEVRYEVCIDIPOCSEVECTCNG 211  
QY 181 ESYRGLMDHTESGKICQWMDHOTPHRHKFLPERRYDCKGDDNVCNRPDQPPRWCYTLDP 240  
DB 212 ESYRGLMDHTESGKICQWMDHOTPHRHKFLPERRYDCKGDDNVCNRPDQPPRWCYTLDP 271  
QY 241 HTRMEYCAIKTCADTMDTVDVPLETTECICQGGEGYRGTVNTWNGICPCQWDSQYPHE 300  
DB 272 HTRMEYCAIKTCADTMDTVDVPLETTECICQGGEGYRGTVNTWNGICPCQWDSQYPHE 331  
QY 301 HMTPEPFCKDRLRENYCENPDGSSPWCFTTDPNIRVGCQIIPNCDSHQDCYRANG 360  
DB 332 HMTPEPFCKDRLRENYCENPDGSSPWCFTTDPNIRVGCQIIPNCDSHQDCYRANG 391  
QY 361 KNYMGNLSQTRSGLTCSMDKXMDLHRHIFWEPDASKLENYCRNPDDAHGPWCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMDKXMDLHRHIFWEPDASKLENYCRNPDDAHGPWCYTGN 451  
QY 421 PLIPMDYCPISRCEGDTPTTIV 442  
DB 452 PLIPMDYCPISRCEGDTPTTIV 473

RESULT 8  
AAR82685  
ID AAR82685 standard; protein; 723 AA.  
XX AAR82685;  
AC AAR82685;  
XX  
XX 24-APR-1996 (first entry)  
DT  
XX  
XX Tumour cytotoxic factor-II.  
DE  
XX Tumour cytotoxic factor-II; TCF-II; hepatocyte growth factor; HGF;  
KW  
XX Monoclonal antibody; MAb; hybridoma; antitumour agent.  
KM  
XX Homo sapiens.  
OS  
XX EP672685-A2.  
XX  
XX 20-SEP-1995.  
PD  
XX 17-MAR-1995; 95EP-00301800.  
PF  
XX 18-MAR-1994; 94JP-00074263.  
PR  
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.  
PA  
XX  
XX Higashio K, Shima N, Oogaki F;  
PI  
XX  
XX WPI; 1995-329569/43.  
DR  
XX Monoclonal antibody to human tumour cytotoxic factor-II - has no affinity  
PT to human hepatocyte growth factor, is used for specific determ. or  
XX purification of TCF-II.  
XX  
XX Disclosure; Page 14-17; 19pp; English.  
XX  
XX This sequence represents human tumour cytotoxic factor-II (TCF-II). TCF-  
CC II has potent antitumour activity and growth stimulation activity. TCF-II  
CC is a member of the hepatocyte growth factor family (HGF). This sequence  
CC is used as an antigen to produce TCF-II specific antibodies that show no  
CC affinity to human HGF. The monoclonal antibody (MAb) was produced using  
CC hybridoma techniques. The MAb were screened using solid phase ELISA with  
CC an increased selectivity. The MAb can be used for the selective  
CC determination or purification of TCF-II without any influence from the  
CC presence of HGF. The TCF-II can be used as an antitumour agent, a wound  
CC healing agent and as a marker for the diagnosis of diseases  
XX  
XX Sequence 723 AA;  
SQ

Query Match 99.9%; Score 2576; DB 2; Length 723;  
Best Local Similarity 99.8%; Pred. No. 1,4e-163;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRRNTIHEPKSAKTTLIKIDPALKIKTKKVTADQCANRCTRNKGLPFTCKAFVFDK 60  
DB :  
DB 32 ORKRRNTIHEPKSAKTTLIKIDPALKIKTKKVTADQCANRCTRNKGLPFTCKAFVFDK 91  
QY 61 ARKQCLMPFNSMSGVKKERGFEDLYENKDYIRNCLIGKRSYKGVSTKSGIKOP 120  
DB 92 ARKQCLMPFNSMSGVKKERGFEDLYENKDYIRNCLIGKRSYKGVSTKSGIKOP 151  
QY 121 WSMIPIHEHSYRGKDLQENYCRNPRGEGGPMCTSNPEVREYECDIPOCSEVECMTCNG 180  
DB 152 WSMIPIHEHSYRGKDLQENYCRNPRGEGGPMCTSNPEVREYECDIPOCSEVECMTCNG 211  
QY 181 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDNVCNPDGQPRPWCYTLD 240  
DB 212 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDNVCNPDGQPRPWCYTLD 271  
QY 241 HTRWEYCAIKTCADNTMNDTVPLETTETCIQOGSGYRGTVNTIWNGLPCQRMDSQYRHE 300  
DB 272 HTRWEYCAIKTCADNTMNDTVPLETTETCIQOGSGYRGTVNTIWNGLPCQRMDSQYRHE 331  
QY 301 HDMPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRNG 360  
DB 332 HDMPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRNG 391  
QY 361 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 451  
QY 421 PLIPWDYCPISRCGDDTTPTIV 442  
DB 452 PLIPWDYCPISRCGDDTTPTIV 473

RESULT 9  
AAW76690  
ID AAW76690 standard; protein; 723 AA.  
XX  
AC AAW76690;  
XX  
AC 25-MAR-2003 (revised)  
DT 29-JAN-1999 (first entry)  
XX  
DE Human plasminogen-like growth factor.  
XX  
KW Human; plasminogen-like growth factor; PLGF; endothelial cell;  
KW epithelial cell; splice variant; wound healing.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 175  
FT /note= "Encoded by ACT"

US8621223-A.  
13-OCT-1998.  
05-MAY-1994; 94US-00238742.  
14-SEP-1990; 90US-00582063.  
(USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Aaronson SA, Rubin JS, Chan AM;  
WPI; 1998-567711/48.  
DR N-PSDB; AAV61952.  
XX

PT Stimulation of endothelial or epithelial cell growth - with plasminogen-  
PT like growth factor protein.  
XX  
PS Claim 3; Fig 4C; 19pp; English.  
XX  
CC The Human plasminogen-like growth factor PLGF is used in the stimulation  
CC of the growth of endothelial cells or epithelial cells other than  
CC hepatocytes. This involves contacting the cells with the PLGF protein or  
CC its allelic or splice variants. The growth factor is useful for  
CC stimulating wound healing in endothelial or epithelial tissue. (Updated  
CC on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 723 AA;

Query Match 99.9%; Score 2576; DB 2; Length 723;  
Best Local Similarity 99.8%; Pred. No. 1,4e-163;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRRNTIHEPKSAKTTLIKIDPALKIKTKKVTADQCANRCTRNKGLPFTCKAFVFDK 60  
DB :  
DB 32 ORKRRNTIHEPKSAKTTLIKIDPALKIKTKKVTADQCANRCTRNKGLPFTCKAFVFDK 91  
QY 61 ARKQCLMPFNSMSGVKKERGFEDLYENKDYIRNCLIGKRSYKGVSTKSGIKOP 120  
DB 92 ARKQCLMPFNSMSGVKKERGFEDLYENKDYIRNCLIGKRSYKGVSTKSGIKOP 151  
QY 121 WSMIPIHEHSYRGKDLQENYCRNPRGEGGPMCTSNPEVREYECDIPOCSEVECMTCNG 180  
DB 152 WSMIPIHEHSYRGKDLQENYCRNPRGEGGPMCTSNPEVREYECDIPOCSEVECMTCNG 211  
QY 181 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDNVCNPDGQPRPWCYTLD 240  
DB 212 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDNVCNPDGQPRPWCYTLD 271  
QY 241 HTRWEYCAIKTCADNTMNDTVPLETTETCIQOGSGYRGTVNTIWNGLPCQRMDSQYRHE 300  
DB 272 HTRWEYCAIKTCADNTMNDTVPLETTETCIQOGSGYRGTVNTIWNGLPCQRMDSQYRHE 331  
QY 301 HDMPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRNG 360  
DB 332 HDMPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRNG 391  
QY 361 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 451  
QY 421 PLIPWDYCPISRCGDDTTPTIV 442  
DB 452 PLIPWDYCPISRCGDDTTPTIV 473

RESULT 10  
AAV06621  
ID AAV06621 standard; protein; 729 AA.  
XX  
AC AAV06621;  
XX  
DT 26-OCT-1999 (first entry)  
XX  
DE HGF-MSP hybrid protein alphabet-1 factor.  
XX  
KW Alphabet-1; human; hepatocyte growth factor; HGF; MSP;  
KW macrophage stimulating protein; apoptosis; chemotherapy; toxicity;  
KW therapy.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Domain 1..487  
FT /note= "HGF alpha chain"  
FT Peptide 1..31  
FT /note= "HSP alpha signal peptide"



FT	Protein	32..729
FT		/note="mature protein"
FT	Cleavage-site	488..491
FT		/note="HGF cleavage site"
FT	Domain	492..717
FT		/note="MSP beta chain"
FT	Peptide	718..729
FT		/note="polyhistidine tag"
XX		
PN	WO9938968-A1.	
XX		
PD	05-AUG-1999.	
XX		
PP	28-JAN-1999;	99WO-EP000502.
XX		
PR	30-JAN-1998;	98IT-MI000180.
XX		
PA	(DOMP-) DOMPE SPA.	
XX		
PI	Medico E, Michieli P, Collesi C, Caselli G, Comoglio P;	
XX		
DR	WPI; 1999-494091/41.	
DR	N-PSDB; AAX87676.	
XX		
PT	Recombinant proteins from recombination of HGF and MSP structural	
PT	domains, useful for protecting cells against apoptosis induced by	
PT	chemotherapeutics.	

Example 1; Page 54-56; 63pp; English.

This is the amino acid sequence of alphabeta-1 factor, a recombinant protein composed of the hepatocyte growth factor (HGF) alpha chain (i.e., the signal sequence, hairpin loop and Kringles 1-4), the natural cleavage site of HGF, the macrophage stimulating protein (MSP) beta chain and a polyhistidine tag sequence. This structure allows the recombinant protein to interact with both the HGF receptor (Met) and the MSP receptor (ron) and thereby induce biological responses which are synergistic and selective compared with the natural factor and truncated forms of the proteins. The portions of DNA encoding the various portions of alphabeta-1 are obtained by PCR amplification of HGF or MSP cDNA and recombined to obtain a hybrid DNA (see AAX87476). Expression vectors, prokaryotic or eukaryotic host cells and a process for preparing recombinant proteins from HGF and MSP are claimed. Alphabeta-1 and other HGF-MSP recombinant proteins are used for the prevention or treatment of chemotherapeutic-induced toxicity such as myelotoxicity, hepatotoxicity, nephrotoxicity, mucotoxicity and neurotoxicity (claimed). They protect cells from death (apoptosis) induced by chemotherapy (e.g., tumors. In particular, they can be used for expansion of marrow precursors, to increase proliferation of the haematopoietic precursors or to stimulate their entry in the cycle. By modification of the proteolytic site, hybrid factors can be obtained which are activated by proteases of the endoplasmic reticulum (such as furins) during their synthesis. When the proteolytic site is removed, permanently immature forms of the factors can be obtained, having a potential partial agonistic or antagonistic activity. Different functional domains can be combined so as to modulate the biological effects

SQ Sequence 729 AA;

Query Match	99.9%	Score 2576;	DB 2;	Length 729;
Best Local Similarity	99.8%	Pred. No. 1.4e-163;		
Matches 441; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 ERKRNTTHEPKSAKTLIKITDPAKIKTKKVNTADOCANCTRKNKGIPFTCAKAVPDK 60  
Db 32 QKRKNTTHEPKSAKTLIKITDPAKIKTKKVNTADOCANCTRKNKGIPFTCAKAVPDK 91  
QY 61 ARKQCLMEPPNMSGSGVKKFEGHEFDLYENKDIYINRCIIIGKGRSYGTVSITSGJICOP 120  
Db 92 ARKQCLMEPPNMSGSGVKKFEGHEFDLYENKDIYINRCIIIGKGRSYGTVSITSGJICOP 151  
QY 121 WSSMTPEHSHYRKGDLQENYCNPRGEGGPMCFSTSNPEVRYEVDIPOCSEVECMTCNG 180

Db	152	WSMSIIEHSHSYNGKQDQENYCNPRGSEGGPMCFISNEEVAEYECDI PQSEVEBCMTG	2111
Qy	181	ESIRGLMDHTESGKICQRMWDHOTPHRHKFLPERYPDKAFDDNNYCRNPDGQRP	2400
Db	212	ESIRGLMDHTESAKICQRMWDHOTPHRHKFLPERYPDKAFDDNNYCRNPDGQRP	2770
Qy	241	HTREWECAIKTCADNMNDTVPLETETSCICQOQSGYGYNTVITWNGIPQCRMSQY	3000
Db	272	HTREWECAIKTCADNMNDTVPLETETSCICQOQSGYGYNTVITWNGIPQCRMSQY	3330
Qy	301	HDMTPEPNFKCKDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDMSHGQD	3660
Db	332	HDMTPEPNFKCKDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDMSHGQD	3990
Qy	361	KNYNGNLISQTSGLTCSMWDKXMEBLHHIITWEPDASKLNNYCRNPDDDAHGPM	4200
Db	392	KNYNGNLISQTSGLTCSMWDKXMEBLHHIITWEPDASKLNNYCRNPDDDAHGPM	4530
Qy	421	PLIPWDYCPISRCGGDTPTTIV 442	
Db	452	PLIPWDYCPISRCGGDTPTTIV 473	

## RESULT 11

ID AAY06622 standard; protein; 729 AA.

AC AAY06622;

DT 26-OCT-1999 (first entry)

DE HGF-MSP hybrid protein alphabet-RTKR factor.

KW Alphabet-RTKR; human; hepatocyte growth factor; HGF; MSP,

KW therapy.

OS Homo sapiens.

XX

FT	Domain	1. .483
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FT	Peptide	1.	.31

FT	Protein	32.	.729	-	-	-
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FT	Cleavage-site	484.	.487

FT	Cleavage-site	488.	.491

FT	Domain	492.717
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FT	Peptide	718.	.729
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DR N-PSDB; AAX87677.

PT Recombinant proteins from recombination of HGF and MSP structural domains, useful for protecting cells against apoptosis induced by

PT chemotherapeutics.  
XX  
XX Example 2; Page 58-60; 63pp; English.  
XX  
CC This is the amino acid sequence of alphabeta-RTK factor, a recombinant  
CC protein composed of the hepatocyte growth factor (HGF) alpha chain (i.e.  
CC the signal sequence, hairpin loop and kringles 1-4), a furine protease  
CC cleavage site, the natural cleavage site of HGF, the macrophage  
CC stimulating protein (MSP) beta chain and a polyhistidine tag sequence.  
CC This structure allows the recombinant protein to interact with both the  
CC HGF receptor (Met) and the MSP receptor (Ron) and thereby induce  
CC biological responses which are synergistic and selective compared with  
CC the natural factor and truncated forms of the proteins. The portions of  
CC DNA encoding the various portions of alphabeta-RTK are obtained by PCR  
CC amplification of HGF or MSP cDNA and recombined to obtain a hybrid DNA  
CC (see AAX87677). Expression vectors, prokaryotic or eukaryotic host cells  
CC and a process for preparing recombinant proteins from HGF and MSP are  
CC claimed. Alphabeta-RTK and other HGF-MSP recombinant proteins are used  
CC for the prevention or treatment of chemotherapeutic-induced toxicity such  
CC as myelotoxicity, hepatotoxicity, nephrotoxicity, mucotoxicity and  
CC neurotoxicity (claimed). They protect cells from death (apoptosis)  
CC induced by chemotherapy of, e.g., tumors. In particular, they can be used  
CC for expansion of marrow precursors, to increase proliferation of the  
CC haematopoietic precursors or to stimulate their entry in the cycle. By  
CC modification of the proteolytic site, hybrid factors can be obtained  
CC which are activated by proteases of the endoplasmic reticulum (such as  
CC furines) during their synthesis. When the proteolytic site is removed,  
CC permanently immature forms of the factors can be obtained, having a  
CC potential partial agonistic or antagonistic activity. Different  
CC functional domains can be combined so as to modulate the biological  
CC effects  
XX  
XX Sequence 729 AA;  
SQ

Query Match 99.9%; Score 2576; DB 2; Length 729;  
Best Local Similarity 99.8%; Pred. No. 1,4e-163;

Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRRNTIHEFKSAKTLIKIDPALKITKKVNTADOCANRCTRNNKLPPTCAFAFVFX 60  
DB 32 QKRRNTIHEFKSAKTLIKIDPALKITKKVNTADOCANRCTRNNKLPPTCAFAFVFX 91  
QY 61 ARKQCLMPFPMSSGSGVKEFGHEFDLYENKDYIRNCIIIGKRSYKGVSTTKSGIKOP 120  
DB 92 ARKQCLMPFPMSSGSGVKEFGHEFDLYENKDYIRNCIIIGKRSYKGVSTTKSGIKOP 151  
QY 121 WSSMIPHEHSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVECMTCNG 180  
DB 152 WSSMIPHEHSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVECMTCNG 211  
QY 181 ESYRGLMDHTESGKICQRWDHQTPIRHKFLPERYPDKGFDNVCNRPDQPRPWCYTLDP 240  
DB 212 ESYRGLMDHTESGKICQRWDHQTPIRHKFLPERYPDKGFDNVCNRPDQPRPWCYTLDP 271  
QY 241 HTRWEYCAIKTCADNTMDTVPLETTTCICQGGEGYGTNTVNTWNGIPQGRWDSQYPHE 300  
DB 272 HTRWEYCAIKTCADNTMDTVPLETTTCICQGGEGYGTNTVNTWNGIPQGRWDSQYPHE 331  
QY 301 HMTPEPNFKCKDLRENYCNRNPDGSGSPMGFTDPPNIRVGCISOIPRCMDSHODCYRNG 360  
DB 332 HMTPEPNFKCKDLRENYCNRNPDGSGSPMGFTDPPNIRVGCISOIPRCMDSHODCYRNG 391  
QY 361 KNYMGNLSQTRSGLTCSMDKMMEDLARIHFWEPDASKLENVCNRPDDAIGPWCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMDKMMEDLARIHFWEPDASKLENVCNRPDDAIGPWCYTGN 451  
QY 421 PLIPMDYCPISRCEGDTPTIIV 442  
DB 452 PLIPMDYCPISRCEGDTPTIIV 473

RESULT 12  
ADD69672

ID ADD69672 standard; protein, 1109 AA.  
XX  
XX AC ADD69672;  
XX  
XX 15-JAN-2004 (first entry)  
XX  
XX DT Chimeric HGF/HBsAg L protein - SEQ ID 20.  
XX  
XX DE Chimeric HGF/HBsAg L protein - SEQ ID 20.  
XX  
XX KW hollow nanoparticle; HBV surface antigen protein; HBsAg L; hepatotropic;  
XX liver disease; gene therapy; chimeric; HGF.  
XX  
XX OS Unidentified.  
XX  
XX OS Hepatitis B virus.  
XX  
XX PN WO2003082345-A1.  
XX  
XX PD 09-OCT-2003.  
XX  
XX PF 05-MAR-2003; 2003WO-JP002602.  
XX  
XX PR 29-MAR-2002; 2002JP-00097280.  
XX  
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX  
XX PI Kuroda S, Tanizawa K, Kondo A, Ueda M, Seno M, Tada H;  
XX  
XX PI WPI, 2003-803976/75.  
XX  
XX DR N-Psdb; ADD69671.  
XX  
XX PT Drugs comprising protein to form hollow nanoparticles with therapeutic  
XX substances encapsulated capable of recognizing target cells or tissues  
XX specifically and selectively, applicable in disease treatment.  
XX  
XX PS Example F; SEQ ID NO 20; 109pp; Japanese.  
XX  
XX CC The invention relates to a novel drug comprising a protein forming hollow  
XX nanoparticles and capable of recognising specific cells which is used  
XX with therapeutic substances for transfer into cells. The protein is  
XX particularly hepatitis B virus (HBV) surface antigen protein (HBsAg). The  
XX drugs of the invention demonstrate hepatotropic activity and may be  
XX useful for disease treatment, particularly in the therapy of liver  
XX diseases. The protein of the invention and subsequently the drug, has  
XX selectivity and specificity in targeting cells or tissues for delivering  
XX drugs fused with the specific nanoparticle-forming proteins, therefore,  
XX gene therapy can be achieved without needing surgery and with reduced  
XX side-effects. The current sequence is that of the chimeric HGF/HBsAg L  
XX protein (SEQ ID 20) of the invention.  
XX  
XX SQ Sequence 1109 AA;

Query Match 99.9%; Score 2576; DB 7; Length 1109;  
Best Local Similarity 99.8%; Pred. No. 2.2e-163;

Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRRNTIHEFKSAKTLIKIDPALKITKKVNTADOCANRCTRNNKLPPTCAFAFVFX 60  
DB 418 QKRRNTIHEFKSAKTLIKIDPALKITKKVNTADOCANRCTRNNKLPPTCAFAFVFX 477  
QY 418 ARKQCLMPFPMSSGSGVKEFGHEFDLYENKDYIRNCIIIGKRSYKGVSTTKSGIKOP 120  
DB 448 ARKQCLMPFPMSSGSGVKEFGHEFDLYENKDYIRNCIIIGKRSYKGVSTTKSGIKOP 151  
QY 478 ARKQCLMPFPMSSGSGVKEFGHEFDLYENKDYIRNCIIIGKRSYKGVSTTKSGIKOP 537  
DB 508 ARKQCLMPFPMSSGSGVKEFGHEFDLYENKDYIRNCIIIGKRSYKGVSTTKSGIKOP 567  
QY 537 WSSMIPHEHSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVECMTCNG 597  
DB 568 WSSMIPHEHSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVCDIPOCSEVECMTCNG 627  
QY 597 ESYRGLMDHTESGKICQRWDHQTPIRHKFLPERYPDKGFDNVCNRPDQPRPWCYTLDP 657  
DB 627 ESYRGLMDHTESGKICQRWDHQTPIRHKFLPERYPDKGFDNVCNRPDQPRPWCYTLDP 687  
QY 657 HTRWEYCAIKTCADNTMDTVPLETTTCICQGGEGYGTNTVNTWNGIPQGRWDSQYPHE 717  
DB 687 HTRWEYCAIKTCADNTMDTVPLETTTCICQGGEGYGTNTVNTWNGIPQGRWDSQYPHE 747

QY 301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGDCYRGNQ 360  
 DB 718 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGDCYRGNQ 777  
 QY 361 KNYMGULSOTRSGLTCSMDKXNMDLHRHIFWEPDASKLNENYCRNPDDAHGPPWCYTGN 420  
 DB 778 KNYMGULSOTRSGLTCSMDKXNMDLHRHIFWEPDASKLNENYCRNPDDAHGPPWCYTGN 837  
 QY 421 PLIPWDYCPISRCGDTPTTIV 442  
 DB 838 PLIPWDYCPISRCGDTPTTIV 859  
 RESULT 13  
 AA57174  
 ID AA57174 standard; protein; 442 AA.  
 AC AA57174;  
 XX  
 DT 11-FEB-2000 (first entry)  
 DE N-terminal region of alpha-chain of HGF mutant (residues 32-478).  
 XX  
 KM Neovascularization; inhibitor; hepatocyte growth factor; HGF;  
 KM cMet-HGF receptor; rheumatoid arthritis; diabetic conjunctivitis;  
 KM neonatal conjunctivitis; senile macular degeneration; scarring; mutant;  
 KM wound healing; contraceptive; vascularization; Crohn's disease; human.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FT Modified-site 1 Location/Qualifiers  
 FT Peptide /note= "pyroglutamate"  
 FT 130..131  
 FT /note= "deletion of 5 amino acids (see AA57173)"  
 PN MO955361-AA.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 06-APR-1999; 99MO-JP001834.  
 XX  
 PR 28-APR-1998; 98JP-00134681.  
 XX  
 PA (NAKA/) NAKAMURA T.  
 XX  
 PI Nakamura T;  
 XX  
 DR WPI; 2000-023263/02.  
 XX  
 PT Neovascularization inhibitory factors and neovascularization inhibitors,  
 PT for preventing or treating, e.g. rheumatoid arthritis and diabetic  
 PT conjunctivitis.  
 XX  
 PS Claim 5; Page 69-72; 78pp; Japanese.  
 XX  
 CC The invention relates to neovascularization inhibitors comprising a  
 CC polypeptide (A) with the amino acid sequence of N-terminal region of  
 CC hepatocyte growth factor (HGF), or a polypeptide with an amino acid  
 CC sequence derived from (A) which has antagonistic activity against HGF via  
 CC the cMet-HGF receptor. The polypeptides can be used as neovascularization  
 CC inhibitory factors (e.g. for preventing and treating rheumatoid  
 CC arthritis, diabetic conjunctivitis, neonatal conjunctivitis, senile  
 CC macular degeneration and excess scarring during wound healing), as a  
 CC contraceptive, to modulate abnormal proliferation or vascularization  
 CC (e.g. psoriasis, Osler-Webber syndrome, myocardiac angiopoiesis,  
 CC peripheral angiectasis, haemophilic rheumatism, angiodysplasia of the eye,  
 CC angiofibroma, benign tumor and wound granulation), or to treat or prevent  
 CC conditions due to the over-stimulation of endothelial cells (e.g. Crohn's  
 CC disease, adenomatous sclerosis, gastrointestinal healing, toughening of  
 CC skin and excess scarring). The present sequence represents the N-terminal

CC region of alpha-chain of human HGF with a deletion of 5 amino acids  
 CC between residues 130 -131 of the present sequence  
 XX  
 SQ Sequence 442 AA;  
 Query Match 99.8%; Score 2574; DB 3; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-163;  
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 RKRRTTIEFFKSAKTTLLKIDPALKIKTKKYNATDOCANRCTRNGKLPFTCAVFDNA 61  
 DB 2 RKRRTTIEFFKSAKTTLLKIDPALKIKTKKYNATDOCANRCTRNGKLPFTCAVFDNA 61  
 QY 62 RKQCLWFPFNSMSGGVKEFGHEFDLYENKDYIRNCIIIGKRSYGTVSITRSIGKQCPW 121  
 DB 62 RKQCLWFPFNSMSGGVKEFGHEFDLYENKDYIRNCIIIGKRSYGTVSITRSIGKQCPW 121  
 QY 122 SSMIPHEHSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCIPQCEVECMTCNCE 181  
 DB 122 SSMIPHEHSYRGKDLQENYCRNPRGEGGWCFTSNPEVRYEVCIPQCEVECMTCNCE 181  
 QY 182 SYRGLMDHTESGKICORMDHOTPHRHKFLPERYPDKGPDNYCRNPDDGPRPWCYTLDPH 241  
 DB 182 SYRGLMDHTESGKICORMDHOTPHRHKFLPERYPDKGPDNYCRNPDDGPRPWCYTLDPH 241  
 QY 242 TWMEYCAIKTCADNTMNDTVDPLETTECIQGGEGYRGTVNTIWNIGIPQCRWDSQYPHEH 301  
 DB 242 TWMEYCAIKTCADNTMNDTVDPLETTECIQGGEGYRGTVNTIWNIGIPQCRWDSQYPHEH 301  
 QY 302 DMTPEPFCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGDCYRGNQ 361  
 DB 302 DMTPEPFCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGDCYRGNQ 361  
 QY 362 NYMGULSOTRSGLTCSMDKXNMDLHRHIFWEPDASKLNENYCRNPDDAHGPPWCYTGNP 421  
 DB 362 NYMGULSOTRSGLTCSMDKXNMDLHRHIFWEPDASKLNENYCRNPDDAHGPPWCYTGNP 421  
 QY 422 LIPWDYCPISRCGDTPTTIV 442  
 DB 422 LIPWDYCPISRCGDTPTTIV 442  
 RESULT 14  
 AAR21142  
 ID AAR21142 standard; protein; 723 AA.  
 XX  
 AC AAR21142;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-MAY-1992 (first entry)  
 XX  
 DE Human TCF-II.  
 XX  
 KW Tumour cell killing factor; hepatocyte growth factor.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT Region 490..505  
 FT /note= "Beta-chain N-terminal sequence"  
 PN WO9201053-A.  
 XX  
 PD 23-JAN-1992.  
 XX  
 PF 13-JUL-1990; 90JP-00185852.  
 XX  
 PR 13-JUL-1990; 90JP-00185852.  
 XX  
 PA (SNOW ) SNOW BRAND MILK PROD CO LTD.  
 XX  
 PI Shima N, Higashio K, Nagao M, Oogaki F, Takaoka H, Tsuda E;  
 XX

DR WPI; 1992-05668/07.  
 DR N-PSDB; AAQ21066.  
 PT Prodn. of liver cell growth factor TCF-II - by culture of a transformant  
 PT contg. cdna for tcf-II and deriving from human foetal lung fibroblast  
 PT cells.  
 XX  
 XX PS Claim 6; Fig 1; 47pp; Japanese.  
 CC A human foetal lung fibroblast library was screened with a synthetic  
 CC probe coding for the N-terminal sequence of TCF-II. A cDNA clone was  
 CC isolated and sequenced. The coding sequence can be incorporated into a  
 CC plasmid and transformed into a microorganism for production of TCF-II.  
 CC The protein itself can be used as a liver cell growth factor or a tumour  
 CC cell killing factor. See also AAQ21067-9. (Updated on 25-MAR-2003 to  
 CC correct PA field.)  
 XX  
 XX Sequence 723 AA;  
 SQ  
 Query Match 99.8%; Score 2573; DB 2; Length 723;  
 Best Local Similarity 99.5%; Pred. No. 2,3e-163;  
 Matches 440; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRNTTHERFKSAKTTLIKIDPAKIKTKKVNNTADOCANCTRNKGLPTCKAFVFDK 60  
 :|||||  
 DB 32 OKRKNNTTHERFKSAKTTLIKIDPAKIKTKKVNNTADOCANCTRNKGLPTCKAFVFDK 91  
 QY 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDIYRNCIIIGKRSYKGVSTITKSGIKOP 120  
 :|||||  
 DB 92 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDIYRNCIIIGKRSYKGVSTITKSGIKOP 151  
 QY 121 WSSMTIPEHSYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCIDIPOCSEVECMTCNG 180  
 :|||||  
 DB 152 WSSMTIPEHSYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCIDIPOCSEVECMTCNG 211  
 QY 181 ESYRGLMDHTESGKICQRMWDHOTPHRHKELPERYPDKGDDNYCRNPDGQPRPWCYTIDP 240  
 :|||||  
 DB 212 ESYRGLMDHTESGKICQRMWDHOTPHRHKELPERYPDKGDDNYCRNPDGQPRPWCYTIDP 271  
 QY 241 HTRWEYCAIKTCADNTMDTVPLETTETCIGOGEGYGTNTVNTWNGIPQCRMSQYRHE 300  
 :|||||  
 DB 272 HTRWEYCAIKTCADNTMDTVPLETTETCIGOGEGYGTNTVNTWNGIPQCRMSQYRHE 331  
 QY 301 HDMTEENFKCDLRENYCRNPDGSESFWCFTTDPNIRVGYCSQIPNCMSHGQDCYRNG 360  
 :|||||  
 DB 332 HDMTEENFKCDLRENYCRNPDGSESFWCFTTDPNIRVGYCSQIPNCMSHGQDCYRNG 391  
 QY 361 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKINENYCRNPDGDAHGPCYTCGN 420  
 :|||||  
 DB 392 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKINENYCRNPDGDAHGPCYTCGN 451  
 QY 421 FLIPMDYCPISRCEGDTPTIV 442  
 :|||||  
 DB 452 FLIPMDYCPISRCEGDTPTIV 473

RESULT 15  
 AAMS59923  
 ID AAMS59923 standard; protein; 723 AA.  
 XX  
 AC AAMS59923;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-DEC-1998 (first entry)  
 XX  
 DE Human leukocyte-derived hepatocyte growth factor HCL2.  
 XX  
 XX Hepatocyte-derived growth factor; HGF; human; liver; hepatoma; diagnosis;  
 XX therapy.  
 OS Homo sapiens.  
 XX  
 PN EP859009-A2.

XX  
 PD 19-AUG-1998.  
 XX  
 XX PF 07-JUN-1991; 98EP-00108130.  
 XX  
 PR 11-JUN-1990; 90JP-00152474.  
 PR 07-JUN-1991; 91EP-00109369.  
 XX  
 XX (NAKAMURA T.  
 XX  
 PI Nakamura T, Hagiya M, Seki T, Shimonishi M, Shimizu S, Ihara I;  
 PI Sakaguchi M, Asami O;  
 DR WPI; 1998-429650/37.  
 DR N-PSDB; AAV53627.  
 XX  
 XX Preparation of recombinant hepatocyte growth factor polypeptide - by  
 PT culturing mammalian cells transformed with vector containing human  
 PT leukocyte-derived HGF gene.  
 XX  
 PS Example 1; Fig 3a-c; 30pp; English.  
 XX  
 CC This is the amino acid sequence for human leukocyte-derived hepatocyte  
 CC growth factor (HGF) HLC2, deduced from a cDNA clone (see AAV53627)  
 CC obtained from a leukocyte cDNA library. Another leukocyte-derived HGF,  
 CC HLC3 (see AAV59924), was identified that differs from HLC3 by having an  
 CC extra 5 amino acid residues. A claimed method of producing a HGF  
 CC recombinant expression vector that has a promoter (preferably the SV40  
 CC early promoter), a gene coding for human leukocyte-derived HGF and the  
 CC dihydrofolate reductase gene; (b) culturing the transformed cells in the  
 CC presence of successively elevated concentrations of methotrexate; and (c)  
 CC recovering the HGF polypeptide from the culture supernatant. HGF  
 CC polypeptides may be used as hepatocyte cultivation reagents, liver  
 CC regeneration promoters, in basic research on liver function, research on  
 CC the action of various hormones and drugs on hepatocytes, research on the  
 CC carcinogenesis mechanism of hepatoma, clinical diagnostic reagents using  
 CC an antibody against the polypeptide and therapeutic drugs for liver  
 CC disease. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR  
 CC -2003 to correct PR field.)  
 XX  
 SQ Sequence 723 AA;  
 Query Match 99.5%; Score 2566; DB 2; Length 723;  
 Best Local Similarity 99.3%; Pred. No. 6,6e-163;  
 Matches 439; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ERKRNTTHERFKSAKTTLIKIDPAKIKTKKVNNTADOCANCTRNKGLPTCKAFVFDK 60  
 :|||||  
 DB 32 OKRKNNTTHERFKSAKTTLIKIDPAKIKTKKVNNTADOCANCTRNKGLPTCKAFVFDK 91  
 QY 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDIYRNCIIIGKRSYKGVSTITKSGIKOP 120  
 :|||||  
 DB 92 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDIYRNCIIIGKRSYKGVSTITKSGIKOP 151  
 QY 121 WSSMTIPEHSYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCIDIPOCSEVECMTCNG 180  
 :|||||  
 DB 152 WSSMTIPEHSYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCIDIPOCSEVECMTCNG 211  
 QY 181 ESYRGLMDHTESGKICQRMWDHOTPHRHKELPERYPDKGDDNYCRNPDGQPRPWCYTIDP 240  
 :|||||  
 DB 212 ESYRGLMDHTESGKICQRMWDHOTPHRHKELPERYPDKGDDNYCRNPDGQPRPWCYTIDP 271  
 QY 241 HTRWEYCAIKTCADNTMDTVPLETTETCIGOGEGYGTNTVNTWNGIPQCRMSQYRHE 300  
 :|||||  
 DB 272 HTRWEYCAIKTCADNTMDTVPLETTETCIGOGEGYGTNTVNTWNGIPQCRMSQYRHE 331  
 QY 301 HDMTEENFKCDLRENYCRNPDGSESFWCFTTDPNIRVGYCSQIPNCMSHGQDCYRNG 360  
 :|||||  
 DB 332 HDMTEENFKCDLRENYCRNPDGSESFWCFTTDPNIRVGYCSQIPNCMSHGQDCYRNG 391  
 QY 361 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKINENYCRNPDGDAHGPCYTCGN 420  
 :|||||

Db	392	KNYMGNLSQTRSGLTCSIMDKNMEDJHRHIFWEPPDASKLNENTCRNPDDDAHGPWCYGN	451
Qy	421	PLIPWDYCPISRCBGDTTPRIV	442
Db	452	PLIPWDYCPISRCBGDTTPRIV	473

Search completed: October 3, 2005, 06:05:51  
job time : 171.535 secs

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QY 121 WSSMIPHEHSYRGKDLQENYCNPRGEGGPMCFINSPEVRYEVCIDIQCSEVECMTCNG 180  
DB 152 WSSMIPHEHSYRGKDLQENYCNPRGEGGPMCFINSPEVRYEVCIDIQCSEVECMTCNG 211  
QY 181 ESYRGLMDHTESGKICQRMWDHOTPHRHKFLPERYPDKGDDNYCNRPDGQPRPWCYTLD 240  
DB 212 ESYRGLMDHTESGKICQRMWDHOTPHRHKFLPERYPDKGDDNYCNRPDGQPRPWCYTLD 271  
QY 241 HTRMEYCAIKTCADNTMNDTVPLETTETCIGQGEGYGTNTTNGIIPCORWDSQYPHE 300  
DB 272 HTRMEYCAIKTCADNTMNDTVPLETTETCIGQGEGYGTNTTNGIIPCORWDSQYPHE 331  
QY 301 HDMTEPNFKCDLRENYCNRPDGSSPMCFITDPNIRVGYCSQIPNCDSHGQDCYRGNG 360  
DB 332 HDMTEPNFKCDLRENYCNRPDGSSPMCFITDPNIRVGYCSQIPNCDSHGQDCYRGNG 391  
QY 361 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCNRPDDAHGPMCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCNRPDDAHGPMCYTGN 451  
QY 421 PLIPWDYCPISRCGDDTTPTIV 442  
DB 452 PLIPWDYCPISRCGDDTTPTIV 473

RESULT 2  
US-08-605-221-4  
; Sequence 4, Application US/08605221  
; Publication No. US20030060403A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, Toshikazu  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE  
; FILE REFERENCE: 2520-0101P  
; CURRENT APPLICATION NUMBER: US/08/605,221  
; CURRENT FILING DATE: 1996-03-15  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: HGF-B (five amino acids deletion type)  
US-08-605-221-4

Query Match 99.9%; Score 2576; DB 8; Length 723;  
Best Local Similarity 99.8%; Pred. No. 1.5e-209;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EKKRRNTIHEFKSAKTLIKIDPALKITKKVNTADQCANRCTRNKGLPTCKAFVFDK 60  
DB 32 QKRRNTIHEFKSAKTLIKIDPALKITKKVNTADQCANRCTRNKGLPTCKAFVFDK 91  
QY 61 ARKQCLMPFPNMSGGVKKEFGEHFDLYENKDYIRNCIIIGKRSYKGVSTIKSGIKOP 120  
DB 92 ARKQCLMPFPNMSGGVKKEFGEHFDLYENKDYIRNCIIIGKRSYKGVSTIKSGIKOP 151  
QY 121 WSSMIPHEHSYRGKDLQENYCNPRGEGGPMCFINSPEVRYEVCIDIQCSEVECMTCNG 180  
DB 152 WSSMIPHEHSYRGKDLQENYCNPRGEGGPMCFINSPEVRYEVCIDIQCSEVECMTCNG 211  
QY 181 ESYRGLMDHTESGKICQRMWDHOTPHRHKFLPERYPDKGDDNYCNRPDGQPRPWCYTLD 240  
DB 212 ESYRGLMDHTESGKICQRMWDHOTPHRHKFLPERYPDKGDDNYCNRPDGQPRPWCYTLD 271  
QY 241 HTRMEYCAIKTCADNTMNDTVPLETTETCIGQGEGYGTNTTNGIIPCORWDSQYPHE 300  
DB 272 HTRMEYCAIKTCADNTMNDTVPLETTETCIGQGEGYGTNTTNGIIPCORWDSQYPHE 331  
QY 301 HDMTEPNFKCDLRENYCNRPDGSSPMCFITDPNIRVGYCSQIPNCDSHGQDCYRGNG 360  
DB 332 HDMTEPNFKCDLRENYCNRPDGSSPMCFITDPNIRVGYCSQIPNCDSHGQDCYRGNG 391  
QY 361 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCNRPDDAHGPMCYTGN 420

DB 392 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCNRPDDAHGPMCYTGN 451  
QY 421 PLIPWDYCPISRCGDDTTPTIV 442  
DB 452 PLIPWDYCPISRCGDDTTPTIV 473

RESULT 3  
US-10-509-247A-20  
; Sequence 20, Application US/10509247A  
; Publication No. US20050181064A1  
; GENERAL INFORMATION:  
; APPLICANT: Japan Science and Technology Corporation  
; APPLICANT: Kuroda, Shunichi  
; APPLICANT: Tanizawa, Katsuyuki  
; APPLICANT: Kondo, Akihiko  
; APPLICANT: Ueda, Masakazu  
; APPLICANT: Sano, Masaharu  
; APPLICANT: Tada, Hiroko  
; TITLE OF INVENTION: DRUG CONTAINING HOLLOW PROTEIN NANOPARTICLES OF PARTICLE-FORMING  
; FILE REFERENCE: P023P01/US  
; CURRENT APPLICATION NUMBER: US/10/509,247A  
; CURRENT FILING DATE: 2004-03-28  
; PRIOR APPLICATION NUMBER: PCT/JP03/02602  
; PRIOR FILING DATE: 2003-03-05  
; PRIOR APPLICATION NUMBER: JP2002-97280  
; PRIOR FILING DATE: 2002-03-29  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20  
; LENGTH: 1109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-509-247A-20

Query Match 99.9%; Score 2576; DB 18; Length 1109;  
Best Local Similarity 99.8%; Pred. No. 2.6e-209;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EKKRRNTIHEFKSAKTLIKIDPALKITKKVNTADQCANRCTRNKGLPTCKAFVFDK 60  
DB 418 QKRRNTIHEFKSAKTLIKIDPALKITKKVNTADQCANRCTRNKGLPTCKAFVFDK 477  
QY 61 ARKQCLMPFPNMSGGVKKEFGEHFDLYENKDYIRNCIIIGKRSYKGVSTIKSGIKOP 120  
DB 478 ARKQCLMPFPNMSGGVKKEFGEHFDLYENKDYIRNCIIIGKRSYKGVSTIKSGIKOP 537  
QY 121 WSSMIPHEHSYRGKDLQENYCNPRGEGGPMCFINSPEVRYEVCIDIQCSEVECMTCNG 180  
DB 538 WSSMIPHEHSYRGKDLQENYCNPRGEGGPMCFINSPEVRYEVCIDIQCSEVECMTCNG 597  
QY 181 ESYRGLMDHTESGKICQRMWDHOTPHRHKFLPERYPDKGDDNYCNRPDGQPRPWCYTLD 240  
DB 598 ESYRGLMDHTESGKICQRMWDHOTPHRHKFLPERYPDKGDDNYCNRPDGQPRPWCYTLD 657  
QY 241 HTRMEYCAIKTCADNTMNDTVPLETTETCIGQGEGYGTNTTNGIIPCORWDSQYPHE 300  
DB 658 HTRMEYCAIKTCADNTMNDTVPLETTETCIGQGEGYGTNTTNGIIPCORWDSQYPHE 717  
QY 301 HDMTEPNFKCDLRENYCNRPDGSSPMCFITDPNIRVGYCSQIPNCDSHGQDCYRGNG 360  
DB 718 HDMTEPNFKCDLRENYCNRPDGSSPMCFITDPNIRVGYCSQIPNCDSHGQDCYRGNG 777  
QY 361 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCNRPDDAHGPMCYTGN 420  
DB 778 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCNRPDDAHGPMCYTGN 837  
QY 421 PLIPWDYCPISRCGDDTTPTIV 442



Db 838 PULPMDYCPISRCEGDTPTIV 859

RESULT 4

US-09-951-629-1  
Sequence 1, Application US/09951629  
Publication No. US20020004480A1

GENERAL INFORMATION:

APPLICANT: NAKAMURA, Toshikazu

TITLE OF INVENTION: Anti-Cancer Agent

FILE REFERENCE: 4373-0101P

CURRENT APPLICATION NUMBER: US/09/951,629

PRIOR FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: JP 300728

PRIOR FILING DATE: 1995-10-24

PRIOR APPLICATION NUMBER: PCT/JP96/03105

PRIOR FILING DATE: 1996-10-23

PRIOR APPLICATION NUMBER: US 09/471,032

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 447

TYPE: PRT

ORGANISM: Homo sapiens

US-09-951-629-1

Query Match 99.4%; Score 2563.5; DB 9; Length 447;  
Best Local Similarity 98.7%; Pred. No. 9.9e-209;

Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 ERKRRNTIHEFKSAKTLIKIDPALKITKKNVNTADQCANRCTRNGKLPFTCKAFVFDK 60

Db 1 ORRRNTIHEFKSAKTLIKIDPALKITKKNVNTADQCANRCTRNGKLPFTCKAFVFDK 60

QY 61 ARKQCLMFPNNSSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKCOP 120

Db 61 ARKQCLMFPNNSSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKCOP 120

QY 121 WSMIPIHEH-----SYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCIDIPOCSEVEC 175

Db 121 WSMIPIHEHFLPSYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCIDIPOCSEVEC 180

QY 176 MTCNGESYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCIDIPOCSEVEC 235

Db 176 MTCNGESYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCIDIPOCSEVEC 240

QY 236 YTLDPHTREYCAIKTCADNTMNDTVPLETTETCIGQGEGRYGVNTIWMGIPCORWDS 295

Db 241 YTLDPHTREYCAIKTCADNTMNDTVPLETTETCIGQGEGRYGVNTIWMGIPCORWDS 300

QY 296 QVPEHDMTPENFKCKDLRENYCRNPDGSESFWCTTDPNIRGYCSOI PNCMSHGDC 355

Db 301 QVPEHDMTPENFKCKDLRENYCRNPDGSESFWCTTDPNIRGYCSOI PNCMSHGDC 360

QY 356 YGNGKNYVGNLSQTRSGLTCSWMDKNMEDLHRHIFWEPDASKLNNYCRNPDDAHGPW 415

Db 361 YGNGKNYVGNLSQTRSGLTCSWMDKNMEDLHRHIFWEPDASKLNNYCRNPDDAHGPW 420

QY 416 CTTGNPLIPWDYCPISRCEGDTPTIV 442

Db 421 CTTGNPLIPWDYCPISRCEGDTPTIV 447

RESULT 5

US-10-081-309-2  
Sequence 2, Application US/10081309  
Publication No. US20030012715A1

GENERAL INFORMATION:

APPLICANT: Hoffmann-La Roche Inc.

TITLE OF INVENTION: PEG Conjugates of NK4

FILE REFERENCE: 20859

CURRENT APPLICATION NUMBER: US/10/081,309

CURRENT FILING DATE: 2002-06-04

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 447

TYPE: PRT

ORGANISM: homosapiens

US-10-081-309-2

Query Match 99.4%; Score 2563.5; DB 14; Length 447;  
Best Local Similarity 98.7%; Pred. No. 9.9e-209;

Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 ERKRRNTIHEFKSAKTLIKIDPALKITKKNVNTADQCANRCTRNGKLPFTCKAFVFDK 60

Db 1 ORRRNTIHEFKSAKTLIKIDPALKITKKNVNTADQCANRCTRNGKLPFTCKAFVFDK 60

QY 61 ARKQCLMFPNNSSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKCOP 120

Db 61 ARKQCLMFPNNSSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKCOP 120

QY 121 WSMIPIHEH-----SYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCIDIPOCSEVEC 175

Db 121 WSMIPIHEHFLPSYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCIDIPOCSEVEC 180

QY 176 MTCNGESYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCIDIPOCSEVEC 235

Db 176 MTCNGESYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCIDIPOCSEVEC 240

QY 236 YTLDPHTREYCAIKTCADNTMNDTVPLETTETCIGQGEGRYGVNTIWMGIPCORWDS 295

Db 241 YTLDPHTREYCAIKTCADNTMNDTVPLETTETCIGQGEGRYGVNTIWMGIPCORWDS 300

QY 296 QVPEHDMTPENFKCKDLRENYCRNPDGSESFWCTTDPNIRGYCSOI PNCMSHGDC 355

Db 301 QVPEHDMTPENFKCKDLRENYCRNPDGSESFWCTTDPNIRGYCSOI PNCMSHGDC 360

QY 356 YGNGKNYVGNLSQTRSGLTCSWMDKNMEDLHRHIFWEPDASKLNNYCRNPDDAHGPW 415

Db 361 YGNGKNYVGNLSQTRSGLTCSWMDKNMEDLHRHIFWEPDASKLNNYCRNPDDAHGPW 420

QY 416 CTTGNPLIPWDYCPISRCEGDTPTIV 442

Db 421 CTTGNPLIPWDYCPISRCEGDTPTIV 447

RESULT 6

US-10-926-088A-1  
Sequence 1, Application US/10926088A  
Publication No. US20050164918A1

GENERAL INFORMATION:

APPLICANT: NAKAMURA Toshikazu

APPLICANT: FUKUDA Kazuhito

TITLE OF INVENTION: A segment of glycosylation-deficient HGF alpha-chain

FILE REFERENCE: 2004-1328A/MMC/01736

CURRENT APPLICATION NUMBER: US/10/926,088A

CURRENT FILING DATE: 2004-08-26

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 1

LENGTH: 494

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE:

OTHER INFORMATION: alpha-chain of human hepatocyte growth factor

US-10-926-088A-1

Query Match 99.4%; Score 2563.5; DB 18; Length 494;  
Best Local Similarity 98.7%; Pred. No. 1.1e-208;

Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 ERKRRNTIHEFKSAKTLIKIDPALKITKKNVNTADQCANRCTRNGKLPFTCKAFVFDK 60

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Db 32 QKRRNTTHERKSAKTLIKIDPALKIKTKKVTADOCANRCTRNKGJPFCTCKAFVFDK 91
Qy 61 ARKOCMLFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKOP 120
Db 92 ARKOCMLFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKOP 151
Qy 121 WSMIPIHEH-----SYRGKDLQENYCRNPRGEGGPMCFNSNPEVRYEVCIDIPOCSEVEC 175
Db 152 WSMIPIHEHSLPSSYRGKDLQENYCRNPRGEGGPMCFNSNPEVRYEVCIDIPOCSEVEC 211
Qy 176 MTCGESYRGKDLMTBESGKICQRMWHDQTPHHRKFLPERYPDKGFDNDYCRNPDQPRPWC 235
Db 212 MTCGESYRGKDLMTBESGKICQRMWHDQTPHHRKFLPERYPDKGFDNDYCRNPDQPRPWC 271
Qy 236 YTLDPHTWMEYCAIKTCADNTMNDVPLETTECTIOGGEYRGTVNTIANGICQWRDS 295
Db 272 YTLDPHTWMEYCAIKTCADNTMNDVPLETTECTIOGGEYRGTVNTIANGICQWRDS 331
Qy 296 QYPHEHMTPENFCKDLRENYCRNPDGSESPWCFITDPNIRVGYCSQIIPNCDMSHGQDC 355
Db 332 QYPHEHMTPENFCKDLRENYCRNPDGSESPWCFITDPNIRVGYCSQIIPNCDMSHGQDC 391
Qy 356 YRGNGKXNYMGNLSQTRSGJLTCSMWDXMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 415
Db 392 YRGNGKXNYMGNLSQTRSGJLTCSMWDXMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 451
Qy 416 CYTGNPLIPMDYCPISRCBGDTPTIV 442
Db 452 CYTGNPLIPMDYCPISRCBGDTPTIV 478
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RESULT 7
US-10-872-198-120
; Sequence 120, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOETSMER
; APPLICANT: Ulrich Kettling
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000204
; CURRENT APPLICATION NUMBER: US/10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-120
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Query Match 99.4%; Score 2563.5; DB 17; Length 726;
Best Local Similarity 98.7%; Pred. No. 1.8e-208;
Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;
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Qy 1 ERKRRNTTHERKSAKTLIKIDPALKIKTKKVTADOCANRCTRNKGJPFCTCKAFVFDK 60
Db 30 QKRRNTTHERKSAKTLIKIDPALKIKTKKVTADOCANRCTRNKGJPFCTCKAFVFDK 89
```

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Qy 61 ARKOCMLFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKOP 120
Db 90 ARKOCMLFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKOP 149
Qy 121 WSMIPIHEH-----SYRGKDLQENYCRNPRGEGGPMCFNSNPEVRYEVCIDIPOCSEVEC 175
Db 150 WSMIPIHEHSLPSSYRGKDLQENYCRNPRGEGGPMCFNSNPEVRYEVCIDIPOCSEVEC 209
Qy 176 MTCGESYRGKDLMTBESGKICQRMWHDQTPHHRKFLPERYPDKGFDNDYCRNPDQPRPWC 235
Db 210 MTCGESYRGKDLMTBESGKICQRMWHDQTPHHRKFLPERYPDKGFDNDYCRNPDQPRPWC 269
Qy 236 YTLDPHTWMEYCAIKTCADNTMNDVPLETTECTIOGGEYRGTVNTIANGICQWRDS 295
Db 270 YTLDPHTWMEYCAIKTCADNTMNDVPLETTECTIOGGEYRGTVNTIANGICQWRDS 329
Qy 296 QYPHEHMTPENFCKDLRENYCRNPDGSESPWCFITDPNIRVGYCSQIIPNCDMSHGQDC 355
Db 330 QYPHEHMTPENFCKDLRENYCRNPDGSESPWCFITDPNIRVGYCSQIIPNCDMSHGQDC 389
Qy 356 YRGNGKXNYMGNLSQTRSGJLTCSMWDXMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 415
Db 390 YRGNGKXNYMGNLSQTRSGJLTCSMWDXMEDLHRHIFWEPDASKLNENYCRNPDGDAHGPW 449
Qy 416 CYTGNPLIPMDYCPISRCBGDTPTIV 442
Db 450 CYTGNPLIPMDYCPISRCBGDTPTIV 476
```

```
RESULT 8
US-11-021-951-120
; Sequence 120, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOETSMER, Christian
; APPLICANT: Kettling, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.000205
; CURRENT APPLICATION NUMBER: US/11/021,951
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-120
```

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Query Match 99.4%; Score 2563.5; DB 20; Length 726;
Best Local Similarity 98.7%; Pred. No. 1.8e-208;
Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;
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Qy 1 ERKRRNTTHERKSAKTLIKIDPALKIKTKKVTADOCANRCTRNKGJPFCTCKAFVFDK 60
Db 1 ERKRRNTTHERKSAKTLIKIDPALKIKTKKVTADOCANRCTRNKGJPFCTCKAFVFDK 60
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Db 30 QRRRRTTTFEKKSAKTTLLIKIDPALKITKKNVTADQCANRCTRNGGLPFTCKAFVFDK 89  
QY 61 ARKQCLMPFPNSMSSGVKKEFGHEFDLYENKDIYRNCIIIGKRSYKGTVSITKSGIKCOP 120  
Db 90 ARKQCLMPFPNSMSSGVKKEFGHEFDLYENKDIYRNCIIIGKRSYKGTVSITKSGIKCOP 149  
QY 121 WSSMIPIHEH-----SYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCDIPOCSEVBC 175  
Db 150 WSSMIPIHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCDIPOCSEVBC 209  
QY 176 MTCNGESYGLMDHTESGKICQRMWDQTPRHAKFLPERYDYGKFDNNYCRNPDGQRPWC 235  
Db 210 MTCNGESYGLMDHTESGKICQRMWDQTPRHAKFLPERYDYGKFDNNYCRNPDGQRPWC 269  
QY 236 YTLDPHTRWYCAIKTCADNTMNDTVPLETTTCIOGQEGYRGVTNTIWNGLPCORWDS 295  
Db 270 YTLDPHTRWYCAIKTCADNTMNDTVPLETTTCIOGQEGYRGVTNTIWNGLPCORWDS 329  
QY 296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQI.PNCDSHGQDC 355  
Db 330 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQI.PNCDSHGQDC 389  
QY 356 YRGNGKNYMGNL.SQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLBNENYCRNPDDAHGPW 415  
Db 390 YRGNGKNYMGNL.SQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLBNENYCRNPDDAHGPW 449  
QY 416 CYTGNPLIPWDYCPISRCBGDTTPTTV 442  
Db 450 CYTGNPLIPWDYCPISRCBGDTTPTTV 476

## RESULT 9

US-08-605-221-2  
; Sequence 2, Application US/08605221  
; Publication No. US20030060403A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, Toshikazu  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE  
; FILE REFERENCE: 2520-0101P  
; CURRENT APPLICATION NUMBER: US/08/605,221  
; CURRENT FILING DATE: 1996-03-15  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 728  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: HGF-A (Full length HGF)  
US-08-605-221-2

Query Match 99.4%; Score 2563.5; DB 8; Length 728;  
Best Local Similarity 98.7%; Pred. No. 1.8e-208;  
Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;  
QY 1 EKKRRNTTTFEKKSAKTTLLIKIDPALKITKKNVTADQCANRCTRNGGLPFTCKAFVFDK 60  
Db 32 QRRRRTTTFEKKSAKTTLLIKIDPALKITKKNVTADQCANRCTRNGGLPFTCKAFVFDK 91  
QY 61 ARKQCLMPFPNSMSSGVKKEFGHEFDLYENKDIYRNCIIIGKRSYKGTVSITKSGIKCOP 120  
Db 92 ARKQCLMPFPNSMSSGVKKEFGHEFDLYENKDIYRNCIIIGKRSYKGTVSITKSGIKCOP 151  
QY 121 WSSMIPIHEH-----SYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCDIPOCSEVBC 175  
Db 152 WSSMIPIHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCDIPOCSEVBC 211  
QY 176 MTCNGESYGLMDHTESGKICQRMWDQTPRHAKFLPERYDYGKFDNNYCRNPDGQRPWC 235  
Db 212 MTCNGESYGLMDHTESGKICQRMWDQTPRHAKFLPERYDYGKFDNNYCRNPDGQRPWC 271  
QY 236 YTLDPHTRWYCAIKTCADNTMNDTVPLETTTCIOGQEGYRGVTNTIWNGLPCORWDS 295  
Db 272 YTLDPHTRWYCAIKTCADNTMNDTVPLETTTCIOGQEGYRGVTNTIWNGLPCORWDS 331

QY 296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQI.PNCDSHGQDC 355  
Db 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQI.PNCDSHGQDC 391  
QY 356 YRGNGKNYMGNL.SQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLBNENYCRNPDDAHGPW 415  
Db 392 YRGNGKNYMGNL.SQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLBNENYCRNPDDAHGPW 451  
QY 416 CYTGNPLIPWDYCPISRCBGDTTPTTV 442  
Db 452 CYTGNPLIPWDYCPISRCBGDTTPTTV 478

## RESULT 10

US-10-813-805-10  
; Sequence 10, Application US/10813805  
; Publication No. US20040191902A1  
; GENERAL INFORMATION:  
; APPLICANT: PEIZER INC.  
; APPLICANT: Hambo, John E.  
; APPLICANT: Roach, Marsha L.  
; TITLE OF INVENTION: GROWTH AND DIFFERENTIATION OF STEM CELLS  
; FILE REFERENCE: PC25028A  
; CURRENT APPLICATION NUMBER: US/10/813,805  
; PRIOR FILING DATE: 2004-03-30  
; PRIOR APPLICATION NUMBER: US 60/459,449  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 728  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-813-805-10

Query Match 99.4%; Score 2563.5; DB 16; Length 728;  
Best Local Similarity 98.7%; Pred. No. 1.8e-208;  
Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;  
QY 1 EKKRRNTTTFEKKSAKTTLLIKIDPALKITKKNVTADQCANRCTRNGGLPFTCKAFVFDK 60  
Db 32 QRRRRTTTFEKKSAKTTLLIKIDPALKITKKNVTADQCANRCTRNGGLPFTCKAFVFDK 91  
QY 61 ARKQCLMPFPNSMSSGVKKEFGHEFDLYENKDIYRNCIIIGKRSYKGTVSITKSGIKCOP 120  
Db 92 ARKQCLMPFPNSMSSGVKKEFGHEFDLYENKDIYRNCIIIGKRSYKGTVSITKSGIKCOP 151  
QY 121 WSSMIPIHEH-----SYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCDIPOCSEVBC 175  
Db 152 WSSMIPIHEHSFLPSSYRGKDLQENYCRNPRGEGGFWCFTSNPEVRYEVCDIPOCSEVBC 211  
QY 176 MTCNGESYGLMDHTESGKICQRMWDQTPRHAKFLPERYDYGKFDNNYCRNPDGQRPWC 235  
Db 212 MTCNGESYGLMDHTESGKICQRMWDQTPRHAKFLPERYDYGKFDNNYCRNPDGQRPWC 271  
QY 236 YTLDPHTRWYCAIKTCADNTMNDTVPLETTTCIOGQEGYRGVTNTIWNGLPCORWDS 295  
Db 272 YTLDPHTRWYCAIKTCADNTMNDTVPLETTTCIOGQEGYRGVTNTIWNGLPCORWDS 331  
QY 296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQI.PNCDSHGQDC 355  
Db 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQI.PNCDSHGQDC 391  
QY 356 YRGNGKNYMGNL.SQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLBNENYCRNPDDAHGPW 415  
Db 392 YRGNGKNYMGNL.SQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLBNENYCRNPDDAHGPW 451  
QY 416 CYTGNPLIPWDYCPISRCBGDTTPTTV 442  
Db 452 CYTGNPLIPWDYCPISRCBGDTTPTTV 478

RESULT 11  
US-10-475-616-2  
; Sequence 2, Application US/10475616  
; Publication No. US20040236073A1  
; GENERAL INFORMATION:  
; APPLICANT: Gherard, Ermanno  
; APPLICANT: Blüedell, Daniel  
; APPLICANT: Chigazde, Dmitry Y  
; TITLE OF INVENTION: The NK1 Fragment of Hepatocyte Growth Factor/Scatter  
; TITLE OF INVENTION: Factor (HGF/SF) and Variants Thereof, and Their Use  
; FILE REFERENCE: 2502489-991180  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: PCT/GB02/01941  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: GB 0110430.6  
; PRIOR FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 728  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-475-616-2

Query Match 99.4%; Score 2563.5; DB 16; Length 728;  
Best Local Similarity 98.7%; Pred. No. 1.8e-208;  
Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 ERKRRNTIHEFKSAKTTLIKIDPALKIKTKKVTADQCANCTRNKGLPTCKAFVFDK 60  
DB :|||||  
QY 32 QKRRNTIHEFKSAKTTLIKIDPALKIKTKKVTADQCANCTRNKGLPTCKAFVFDK 91  
DB :|||||  
QY 61 ARKQCLMPFPMSSSGVKKFEGHFDLYENKDIYRNCIIIGKRSYKGVSTIKSGIKOP 120  
DB 92 ARKQCLMPFPMSSSGVKKFEGHFDLYENKDIYRNCIIIGKRSYKGVSTIKSGIKOP 151  
QY 121 WSSMI.PHEH-----SYRGKDLQENYCRNPRGEGGPMCTSNPEVRYEVCIDIPQCEVEVC 175  
DB 152 WSSMI.PHEHSLPSPSYRGKDLQENYCRNPRGEGGPMCTSNPEVRYEVCIDIPQCEVEVC 211  
QY 176 MTCNGESYRGKLDHTESGKICQRMWDHQTPHRHKFLPERYPDXGPDNNYCRNPDQPRPWC 235  
DB 212 MTCNGESYRGKLDHTESGKICQRMWDHQTPHRHKFLPERYPDXGPDNNYCRNPDQPRPWC 271  
QY 236 YTLDPHTRWECALIKTCADNTMNDTVDVLETTTECIIQGGEGYRGVTNTIWMGIPQQRWDS 295  
DB 272 YTLDPHTRWECALIKTCADNTMNDTVDVLETTTECIIQGGEGYRGVTNTIWMGIPQQRWDS 331  
QY 296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGQDC 355  
DB 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGQDC 391  
QY 356 YRGNGKNYMGNL.SQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCRNPDHDAHGPW 415  
DB 392 YRGNGKNYMGNL.SQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCRNPDHDAHGPW 451  
QY 416 CYTGNPLIPWDYCPISRCGSDTPTIV 442  
DB 452 CYTGNPLIPWDYCPISRCGSDTPTIV 478

RESULT 12  
US-10-498-332-7  
; Sequence 7, Application US/10498332  
; Publication No. US20050113284A1  
; GENERAL INFORMATION:  
; APPLICANT: Nakamura, Motoao  
; APPLICANT: Higuchi, Toshio  
; APPLICANT: Yamasaki, Yoshiki  
; APPLICANT: Orita, Takuya  
; TITLE OF INVENTION: PHARMACEUTICAL AGENTS AND METHODS FOR

; TITLE OF INVENTION: TISSUE AND VASCULAR REGENERATION  
; FILE REFERENCE: 14539-016US1  
; CURRENT APPLICATION NUMBER: US/10/498.332  
; CURRENT FILING DATE: 2004-06-11  
; PRIOR APPLICATION NUMBER: PCT/JP02/13014  
; PRIOR FILING DATE: 2002-12-12  
; PRIOR APPLICATION NUMBER: JP 2002-352924  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: JP 2001-380158  
; PRIOR FILING DATE: 2001-12-13  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 728  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-498-332-7

Query Match 99.4%; Score 2563.5; DB 17; Length 728;  
Best Local Similarity 98.7%; Pred. No. 1.8e-208;  
Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 ERKRRNTIHEFKSAKTTLIKIDPALKIKTKKVTADQCANCTRNKGLPTCKAFVFDK 60  
DB :|||||  
QY 32 QKRRNTIHEFKSAKTTLIKIDPALKIKTKKVTADQCANCTRNKGLPTCKAFVFDK 91  
DB :|||||  
QY 61 ARKQCLMPFPMSSSGVKKFEGHFDLYENKDIYRNCIIIGKRSYKGVSTIKSGIKOP 120  
DB 92 ARKQCLMPFPMSSSGVKKFEGHFDLYENKDIYRNCIIIGKRSYKGVSTIKSGIKOP 151  
QY 121 WSSMI.PHEH-----SYRGKDLQENYCRNPRGEGGPMCTSNPEVRYEVCIDIPQCEVEVC 175  
DB 152 WSSMI.PHEHSLPSPSYRGKDLQENYCRNPRGEGGPMCTSNPEVRYEVCIDIPQCEVEVC 211  
QY 176 MTCNGESYRGKLDHTESGKICQRMWDHQTPHRHKFLPERYPDXGPDNNYCRNPDQPRPWC 235  
DB 212 MTCNGESYRGKLDHTESGKICQRMWDHQTPHRHKFLPERYPDXGPDNNYCRNPDQPRPWC 271  
QY 236 YTLDPHTRWECALIKTCADNTMNDTVDVLETTTECIIQGGEGYRGVTNTIWMGIPQQRWDS 295  
DB 272 YTLDPHTRWECALIKTCADNTMNDTVDVLETTTECIIQGGEGYRGVTNTIWMGIPQQRWDS 331  
QY 296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGQDC 355  
DB 332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGQDC 391  
QY 356 YRGNGKNYMGNL.SQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCRNPDHDAHGPW 415  
DB 392 YRGNGKNYMGNL.SQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNENYCRNPDHDAHGPW 451  
QY 416 CYTGNPLIPWDYCPISRCGSDTPTIV 442  
DB 452 CYTGNPLIPWDYCPISRCGSDTPTIV 478

RESULT 13  
US-10-133-912-18  
; Sequence 18, Application US/10133912  
; Publication No. US20020165358A1  
; GENERAL INFORMATION:  
; APPLICANT: Kinoshita, Masahiko  
; APPLICANT: Yamaguchi, Kyoji  
; APPLICANT: Goto, Masaki  
; APPLICANT: Murakami, Akihiko  
; APPLICANT: Ueda, Masatsugu  
; APPLICANT: Higashio, Kanji  
; APPLICANT: Yamauchi, Yasushi  
; TITLE OF INVENTION: TCF MUTANT  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burgess, Ryan and Wayne  
; STREET: 370 Lexington Avenue, Suite 2105  
; CITY: NEW YORK

STATE: NEW YORK  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 10017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/5 inch diskette  
COMPUTER: PC'S LIMITED SYSTEM 200  
OPERATING SYSTEM: WORD FOR WINDOWS  
SOFTWARE: MICROSOFT WINDOWS 98  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/133,912  
FILING DATE: 25-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,519  
FILING DATE: 26-Aug-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Wayne, Milton J.  
REGISTRATION NUMBER: 17,906  
REFERENCE/DOCKET NUMBER: U-Wp-5240PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-683-8150  
TELEFAX: 212-532-4285  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723  
TYPE: AMINO ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-133-912-18

Query Match 99.0%; Score 2554; DB 13; Length 723;  
Best Local Similarity 100.0%; Pred. No. 1.1e-207;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 NTHERKSKAKTLIKIDPALKIKTKKVNADOCANRCTRNKGLPTCKAFVFDKARKQC 65  
DB 37 NTHERKSKAKTLIKIDPALKIKTKKVNADOCANRCTRNKGLPTCKAFVFDKARKQC 96  
QY 66 LMFPPMSMSGVKEFGHEFDLYENKDYINNCIIIGKRSYKGTVSITKSGIKQPMSSMT 125  
DB 97 LMFPPMSMSGVKEFGHEFDLYENKDYINNCIIIGKRSYKGTVSITKSGIKQPMSSMT 156  
QY 126 PHEHSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVDIPQCESEVECTCNCGESYRG 185  
DB 157 PHEHSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVDIPQCESEVECTCNCGESYRG 216  
QY 186 LMDHTSSGKICQWMDHOTPHRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLLDPTTRWE 245  
DB 217 LMDHTSSGKICQWMDHOTPHRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLLDPTTRWE 276  
QY 246 YCAIKTCADNTMDTVPLETTTCIOGQGGYGTVNTIWNGLPCORWDSQYHEHDMTP 305  
DB 277 YCAIKTCADNTMDTVPLETTTCIOGQGGYGTVNTIWNGLPCORWDSQYHEHDMTP 336  
QY 306 ENFKCDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDCYRNGKXNYNG 365  
DB 337 ENFKCDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDCYRNGKXNYNG 396  
QY 366 NLSQTSGLTCSMWDXKMEDLHRHITWEPDASKLNNYCRNPDDAHGPWCYTGNLIPW 425  
DB 397 NLSQTSGLTCSMWDXKMEDLHRHITWEPDASKLNNYCRNPDDAHGPWCYTGNLIPW 456  
QY 426 DYCPIRSRCSGDTPTTIV 442  
DB 457 DYCPIRSRCSGDTPTTIV 473

RESULT 14  
US-10-133-912-19  
Sequence 19: Application US/10133912  
Publication NO: US20020165358A1  
GENERAL INFORMATION:

APPLICANT: Kinoshaki, Masahiko  
Yamaguchi, Kyoji  
Goto, Masaki  
Murakami, Akihiko  
Ueda, Masatsugu  
Higashio, Kanji  
Yamashita, Yasushi  
TITLE OF INVENTION: TCF MUTANT  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burgess, Ryan and Wayne  
STREET: 370 Lexington Avenue, Suite 2105  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 10017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/5 inch diskette  
COMPUTER: PC'S LIMITED SYSTEM 200  
OPERATING SYSTEM: WORD FOR WINDOWS  
SOFTWARE: MICROSOFT WINDOWS 98  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/133,912  
FILING DATE: 25-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,519  
FILING DATE: 26-Aug-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Wayne, Milton J.  
REGISTRATION NUMBER: 17,906  
REFERENCE/DOCKET NUMBER: U-Wp-5240PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-683-8150  
TELEFAX: 212-532-4285  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723  
TYPE: AMINO ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-10-133-912-19

Query Match 99.0%; Score 2552; DB 13; Length 723;  
Best Local Similarity 98.9%; Pred. No. 1.7e-207;  
Matches 437; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ERKRNTIHEFKSKAKTLIKIDPALKIKTKKVNADOCANRCTRNKGLPTCKAFVFDK 60  
DB 32 ERKRNTIHEFKSKAKTLIKIDPALAATAVNTADOCANRCTRNKGLPTCKAFVFDK 91  
QY 61 ARKQCLMPFPNMSGVKEFGHEFDLYENKDYINNCIIIGKRSYKGTVSITKSGIKQCP 120  
DB 92 ARKQCLMPFPNMSGVKEFGHEFDLYENKDYINNCIIIGKRSYKGTVSITKSGIKQCP 151  
QY 121 WSSMTPEHSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVDIPQCESEVECTCNCG 180  
DB 152 WSSMTPEHSYRGKDLQENYCRNPRGEGGPMCFSTNPEVRYEVDIPQCESEVECTCNCG 211  
QY 181 ESYRGLMDHTSSGKICQWMDHOTPHRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLLD 240  
DB 212 ESYRGLMDHTSSGKICQWMDHOTPHRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLLD 271  
QY 241 HTRWEYCAIKTCADNTMDTVPLETTTCIOGQGGYGTVNTIWNGLPCORWDSQYHEH 300  
DB 272 HTRWEYCAIKTCADNTMDTVPLETTTCIOGQGGYGTVNTIWNGLPCORWDSQYHEH 331  
QY 301 HDMTPENFKCDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDCYRNGK 360  
DB 332 HDMTPENFKCDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGQDCYRNGK 391  
QY 361 KNYMGNLSQTSGLTCSMWDXKMEDLHRHITWEPDASKLNNYCRNPDDAHGPWCYTGN 420

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Db      392 KVMNGLSOTRSGLTCSMWKMDKMDLHRHIFWEPDASKLNENYCRNPPDDAHGPMCYTGN 451
QY      421 PLIPWDYCPISRCEGDTTPTIV 442
Db      452 PLIPWDYCPISRCEGDTTPTIV 473

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RESULT 15

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US-10-149-103A-1
; Sequence 1, Application US/10149103A
; Publication No. US20040121945A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Hong
; APPLICANT: Sim, Kim Lee
; APPLICANT: Day, Clara
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
; FILE REFERENCE: 05213-0592 43170-274540
; CURRENT APPLICATION NUMBER: US/10/149,103A
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/US00/34039
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 727
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-149-103A-1

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Query Match 98.0%; Score 2527.5; DB 16; Length 727;  
 Best Local Similarity 97.1%; Pred. No. 2e-205;  
 Matches 433; Conservative 6; Mismatches 2; Indels 5; Gaps 1;

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QY      2 RRRRTTIEFKKSAKTTLIKIDPALKITKRYNTADQCANRCTRNGKLPFTCKAFVFDKA 61
Db      33 KRRRTTIEFKKSAKTTLIKIDPALKITKRYNTADQCANRCTRNGKLPFTCKAFVFDKA 92
QY      62 RQCLMFPPNSMSGVKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITRSGIKQCPW 121
Db      93 RQCLMFPPNSMSGVKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITRSGIKQCPW 152
QY      122 SSMIPHEH-----SYRGKDLQENYCRNPRGEGGPMWCFTSNPEVRYEVCDIPOCSEVECM 176
Db      153 SSMIPHEHGFLLPSYRGKDLQENYCRNPRGEGGPMWCFTSNPEVRYEVCDIPOCSEVECM 212
QY      177 TNGSSYRGLMDHTESGKICQRMWDHOTPHRHKFLPERYPDKGFDQDYCRNPDGQRPWPCY 236
Db      213 TNGSSYRGLMDHTESGKICQRMWDHOTPHRHKFLPERYPDKGFDQDYCRNPDGQRPWPCY 272
QY      237 TLDPHTREYCAIKTCADNTMNDTVPLBTEECIOGQEGYRGTVNTINNGIPCORWDSQ 296
Db      273 TLDPHTREYCAIKTCADNTMNDTVPLBTEECIOGQEGYRGTVNTINNGIPCORWDSQ 332
QY      297 YPHEHDMTPENFKCXDLRENYCRNPDGSESPMWCFITDPNIRVGYCSQIPNCDSHGOQCY 356
Db      333 YPHKIDMTPENFCKXDLRENYCRNPDGSESPMWCFITDPNIRVGYCSQIPNCDSHGOQCY 392
QY      357 RGNKRYMGNLSOTRSGLTCSMWKMDKMDLHRHIFWEPDASKLNENYCRNPPDDAHGPMW 416
Db      393 RGNKRYMGNLSOTRSGLTCSMWKMDKMDLHRHIFWEPDASKLNENYCRNPPDDAHGPMW 452
QY      417 YTGNPPLIPWDYCPISRCEGDTTPTIV 442
Db      453 YTGNPPLIPWDYCPISRCEGDTTPTIV 478

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 Job time : 239.645 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:32 : Search time 1360.31 Seconds  
(without alignments)  
24.255 Million cell updates/sec

Title: US-09-674-377B-2

Perfect score: 2579  
Sequence: 1 EKKRRNTIHEFKKSAKTTLI.....IPWDYCPISRCBGDTTPRTIV 442

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2576	99.9	487	4	US-09-601-040A-27
2	2576	99.9	717	4	US-09-601-040A-6
3	2576	99.9	717	4	US-09-601-040A-8
4	2576	99.9	723	1	US-07-838-410-1
5	2576	99.9	723	1	US-08-290-937B-1
6	2576	99.9	723	1	US-08-290-937B-2
7	2576	99.9	723	1	US-08-404-643-1
8	2576	99.9	723	3	US-09-194-326-1
9	2576	99.9	723	4	US-09-600-991-18
10	2576	99.9	723	4	US-08-605-921-4
11	2576	99.9	723	4	US-09-601-040A-10
12	2576	99.9	723	4	US-09-601-040A-2
13	2576	99.9	729	4	US-09-601-040A-4
14	2573	99.8	723	3	US-08-030-810-3
15	2570	99.7	723	3	US-08-290-937B-3
16	2563.5	99.4	697	2	US-08-460-890A-50
17	2563.5	99.4	697	2	US-08-167-641C-50
18	2563.5	99.4	697	3	US-08-460-971A-50
19	2563.5	99.4	697	3	US-08-462-040-50
20	2563.5	99.4	728	1	US-07-815-333A-2
21	2563.5	99.4	728	4	US-08-087-783A-22
22	2563.5	99.4	728	4	US-08-605-221-2
23	2554	99.0	723	3	US-09-194-326-2
24	2554	99.0	723	3	US-08-700-519J-18
25	2552	99.0	723	3	US-09-194-326-3
26	2552	99.0	723	3	US-08-700-519J-19
27	1793	69.5	574	4	US-09-600-991-2

28	1460	56.6	563	4	US-09-600-991-4	Sequence 4, Appl1
29	1433.5	55.6	290	4	US-08-484-841A-8	Sequence 8, Appl1
30	1171	45.4	711	1	US-08-184-012C-8	Sequence 2, Appl1
31	1171	45.4	711	1	US-08-334-177-2	Sequence 1, Appl1
32	1171	45.4	711	2	US-08-666-082B-1	Sequence 2, Appl1
33	1171	45.4	711	2	US-08-766-982-2	Sequence 2, Appl1
34	1171	45.4	711	3	US-09-296-219-2	Sequence 2, Appl1
35	1171	45.4	711	4	US-09-600-991-20	Sequence 20, Appl1
36	1171	45.4	711	4	US-09-601-040A-12	Sequence 12, Appl1
37	1171	45.4	711	4	US-09-949-016-6981	Sequence 6981, Ap
38	1171	45.4	711	5	PCT-US95-13830-2	Sequence 2, Appl1
39	1114.5	43.2	716	3	US-08-766-982-1	Sequence 1, Appl1
40	1114.5	43.2	716	2	US-09-296-219-1	Sequence 1, Appl1
41	1054.5	40.9	790	4	US-08-991-761A-13	Sequence 13, Appl1
42	1039.5	40.3	812	1	US-08-248-629A-1	Sequence 1, Appl1
43	1039.5	40.3	812	1	US-08-451-932-1	Sequence 1, Appl1
44	1039.5	40.3	812	1	US-08-452-260-1	Sequence 1, Appl1
45	1039.5	40.3	812	1	US-08-326-785-1	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-601-040A-27  
; Sequence 27, Application US/09601040A  
; Patent No. 6730657  
; GENERAL INFORMATION:  
; APPLICANT: MEDICO, Enzo et al.  
; TITLE OF INVENTION: Recombinant Proteins from HGF and MSP  
; FILE REFERENCE: 0471-0161P  
; CURRENT APPLICATION NUMBER: US/09/601,040A  
; CURRENT FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27  
; LENGTH: 487  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-601-040A-27

Query Match 99.9%; Score 2576; DB 4; Length 487;  
Best Local Similarity 99.8%; Pred. No. 1.1e-213;

Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	EKKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVTADOCANRCTNKGLPFTCKAFVPPK	60
DB	32	QKKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVTADOCANRCTNKGLPFTCKAFVPPK	91
QY	61	ARKQCIWPFPPNMSGSKVKEFGHEFDLYENKDIYINNCIIIGKRSYKGVISITKSGIKCOP	120
DB	92	ARKQCIWPFPPNMSGSKVKEFGHEFDLYENKDIYINNCIIIGKRSYKGVISITKSGIKCOP	151
QY	121	WSSMTIPHEHSYKGLQENYCNRPGEBCGPMCFPSNPEVYECVDIPCCSEVECTCNG	180
DB	152	WSSMTIPHEHSYKGLQENYCNRPGEBCGPMCFPSNPEVYECVDIPCCSEVECTCNG	211
QY	181	ESYRGIMDTESGKICQRMHDQTPRHKFLPRRYDCKGDDVYCNRPDQPPWCYTLP	240
DB	212	ESYRGIMDTESGKICQRMHDQTPRHKFLPRRYDCKGDDVYCNRPDQPPWCYTLP	271
QY	241	HTRWECALIKTCADYMDTDVPLETTECTIOQSGEGYRGTVNTIWNGLPCQRMDSQYPIE	300
DB	272	HTRWECALIKTCADYMDTDVPLETTECTIOQSGEGYRGTVNTIWNGLPCQRMDSQYPIE	331
QY	301	HMTBENFCKDLRENYCNRPDGSPPMCFITDPIRNGYCSQIIPNCMSHQDCYRNG	360
DB	332	HMTBENFCKDLRENYCNRPDGSPPMCFITDPIRNGYCSQIIPNCMSHQDCYRNG	391
QY	361	KYMGGLSOTRSGGLCSMWDKMDLHRIIPEWPASKLNEYCNRPDDAGPWCYTGN	420
DB	392	KYMGGLSOTRSGGLCSMWDKMDLHRIIPEWPASKLNEYCNRPDDAGPWCYTGN	451

```
QY      421 PLIPWDYCPISRCEGDTTPTIV 442  
         |||||  
Db     452 PLIPWDCPISRCEGDTPITIV 473
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## RESULT 2

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US-09-601-040A-6
; Sequence 6, Application US/09601040A
; Patent No. 6730657
; GENERAL INFORMATION:
; APPLICANT: MEDICO, Enzo et al.
; TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
; FILE REFERENCE: 0471-0161p
; CURRENT APPLICATION NUMBER: US/09/601,040A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 717
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant sequence derived from Homo sapiens
US-09-601-040A-6

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Query Match	99.9%;	Score 2576;	DB 4;	Length 717;
Best Local Similarity	99.8%;	Pred. No. 1.8e-213;		
Matches 441;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	ERRKRNTIHEFFKSASATLLIKIDPAKIKTKKVTNADOCARCTRNKGLPTTCAPFDK	60
Dp	32	QRRKRNTIHEFFKSASATLLIKIDPAKIKTKKVTNADOCARCTRNKGLPTTCAPFDK	91
Qy	61	ARKQCLMFPNMSMSGYKKEFGHEPDLYENKOYIRNCIIIGKRSYKGVSTITSKGIKOP	120
Dp	92	ARKQCLMFPNMSMSGYKKEFGHEPDLYENKOYIRNCIIIGKRSYKGVSTITSKGIKOP	151
Qy	121	WSSMIPIHEHSYRKDLOENYCRNPROBEGPWCFTSNPEVRYEVDIQCSEVECMONG	180
Dp	152	WSSMIPIHEHSYRKDLOENYCRNPROBEGPWCFTSNPEVRYEVDIQCSEVECMONG	211
Qy	181	ESYRGLMDHTESGKICORDMDQTPHRAKELPERYPDKGFDNDCRNPDGQRPWCYTILDP	240
Dp	212	ESYRGLMDHTESGKICORDMDQTPHRAKELPERYPDKGFDNDCRNPDGQRPWCYTILDP	271
Qy	241	HTREYCAITTCADNMNDTDVLETTBEICIQOGSEYRGTVNTIINGIIPCRNMSQYVPE	300
Dp	272	HTREYCAITTCADNMNDTDVLETTBEICIQOGSEYRGTVNTIINGIIPCRNMSQYVPE	331
Qy	301	HDMPENFKCDLRENYCRNPDGSESPMCFTTDPNIRVYCSQIPNCMSHGQDCYRNG	360
Dp	332	HDMPENFKCDLRENYCRNPDGSESPMCFTTDPNIRVYCSQIPNCMSHGQDCYRNG	391
Qy	361	KNYVGNISQTRSGJLTCSMMDKNMEDLHRII FWEPDASKLENYCRNPDDAHGWCYTGN	420
Dp	392	KNYVGNISQTRSGJLTCSMMDKNMEDLHRII FWEPDASKLENYCRNPDDAHGWCYTGN	451
Qy	421	PLIPMDYCPISRCBGDTPTTIV 442	
Dp	452	PLIPMDYCPISRCBGDTPTTIV 473	

### RESULT 3

```

1  US-09-601-040A-8
2  Sequence 8, Application US/09601040A
3  Patent No. 6730657
4  GENERAL INFORMATION:
5  APPLICANT: MEDICO, Enzo et al.
6  TITLE OF INVENTION: Recombinant Proteins from HGF and MSF
7  FILE REFERENCE: 0471-0161P
8  CURRENT APPLICATION NUMBER: US/09/601,040A
9  CURRENT FILING DATE: 2000-09-08
10 NUMBER OF SEQ ID NOS: 28

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? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 8
? LENGTH: 717
? TYPE: prt
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Recombinant sequence derived from Homo sapiens
?S-09-601-040A-8

```

Query Match	99.9%	Score 2576;	DB 4;	Length 717;
Best Local Similarity	99.8%	Pred. No. 1.8e-213;		
Matches 441; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	ERRRRNTTIEFPKSAKTLIKIDPALKIKTKKVVNTADOCANRCTRNKGLPFTCAFEYFDK	60
Db	32	QRRRRNTTIEFPKSAKTLIKIDPALKIKTKKVVNTADOCANRCTRNKGLPFTCAFEYFDK	91
Qy	61	ARKQCLMPFPNMSGGVKKFEGHEFDLYENKDYIRNCLIGKRSYKGTVAITYSGIKCOP	120
Db	92	ARKQCLMPFPNMSGGVKKFEGHEFDLYENKDYIRNCLIGKRSYKGTVAITYSGIKCOP	151
Qy	121	WSMNTIPIHESYNGKLOENYCRNPGEGBGWCSTSNPEURYEVKCDIPOSSEVCMTNG	180
Db	152	WSMNTIPIHESYNGKLOENYCRNPGEGBGWCSTSNPEURYEVKCDIPOSSEVCMTNG	211
Qy	181	ESYRGIMDTBESGKICQRMWDQTPRHAKFLBERYPDGFQPDNYCRNPDCQPRPWCYTLDP	240
Db	212	ESYRGIMDTBESGKICQRMWDQTPRHAKFLBERYPDGFQPDNYCRNPDCQPRPWCYTLDP	271
Qy	241	HTRWECALKTCAADTAMDYDVPLETTBECIOGQGBRGTVNTIANGICPORNDSDYPIHE	300
Db	272	HTRWECALKTCAADTAMDYDVPLETTBECIOGQGBRGTVNTIANGICPORNDSDYPIHE	331
Qy	301	HDWTPENFKCLOLRNRCRNPDSGSPKCFITTDNIRIGVCSQIPNCMDSMHGGDCYRNG	360
Db	332	HDWTPENFKCLOLRNRCRNPDSGSPKCFITTDNIRIGVCSQIPNCMDSMHGGDCYRNG	391
Qy	361	KNYMGNTLSOTRSGLTCSMWDKMKBELHRIHFWBPDAKLTENYCRNPDDDAHGWPCYTN	420
Db	392	KNYMGNTLSOTRSGLTCSMWDKMKBELHRIHFWBPDAKLTENYCRNPDDDAHGWPCYTN	451
Qy	421	PLIPMDYCPISRCBGDTTPTIV	442
Db	452	PLIPMDYCPISRCBGDTTPTIV	473

## RESULT 4

US-07-838-410-1  
Sequence 1, Application US/07838410  
Patent No. 5328836  
GENERAL INFORMATION:  
APPLICANT: SHIMA, NOBUYUKI  
APPLICANT: HIGASHIO, KANJI  
APPLICANT: NAGAO, MASAYA  
APPLICANT: OGAKI, FUMIKO  
APPLICANT: TAKAKURA, HIROAKI  
APPLICANT: TSUDA, EISUKE  
TITLE OF INVENTION: PLASMIDS CONTAINING DNA ENCODING THE  
TITLE OF INVENTION: AMINO ACID SEQUENCE OF TCF-II, TRANSFORMED CELLS WITH THE  
TITLE OF INVENTION: PLASMIDS, AND PRODUCTION METHOD OF BIOLOGICALLY ACTIVE  
SUBSTANCE USING THE TRANSFORMED CELLS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD.  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS



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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/838,410
FILING DATE: 19920311
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00942
FILING DATE: 15-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185852-1990
FILING DATE: 13-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN L.
REGISTRATION NUMBER: 17,746
REFERENCE/DOCKET NUMBER: WAK 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Fibroblast
FEATURE:
NAME/KEY: Domain
LOCATION: 393..405
OTHER INFORMATION: /note= "INTERNAL AMINO ACID"
FEATURE:
NAME/KEY: Protein
LOCATION: 490..505
OTHER INFORMATION: /note= "N-TERMINAL AMINO ACID"
OTHER INFORMATION: SEQUENCE OF BETA-CHAIN"
FEATURE:
NAME/KEY: Domain
LOCATION: 605..623
OTHER INFORMATION: /note= "INTERNAL AMINO ACID"
OTHER INFORMATION: SEQUENCE IN BETA-CHAIN"
US-07-838-410-1

Query Match      99.9%; Score 2576; DB 1; Length 723;
Best Local Similarity 99.8%; Pred. No. 1.9e-213;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRRTIHEFKSAKTTLLIKIDPALKITKRVNTADOCANRCTRNKGLPFTCKAFVFPK 60
DB 32 QRRKRTIHEFKSAKTTLLIKIDPALKITKRVNTADOCANRCTRNKGLPFTCKAFVFPK 91
QY 61 ARKQCLMPFPNSMSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKCOP 120
DB 92 ARKQCLMPFPNSMSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKCOP 151
QY 121 WSSMIPIHEHSYRKDIOENYCNRPGBEGGPMCFTSNPEVRYEVCDIPOCSEVECTCNG 180
DB 152 WSSMIPIHEHSYRKDIOENYCNRPGBEGGPMCFTSNPEVRYEVCDIPOCSEVECTCNG 211
QY 181 ESFRGLMDHTESGKICORMDHOTPHRHKFLPERYPDKGFPDNYCRNPDGQPRMCTTLP 240
DB 212 ESFRGLMDHTESGKICORMDHOTPHRHKFLPERYPDKGFPDNYCRNPDGQPRMCTTLP 271
QY 241 HTRWEYCAIKTCADNTMNDTVPLEETECTIQGGEGYRGTVNTIWMGIPQQRWDSQYPHE 300
DB 272 HTRWEYCAIKTCADNTMNDTVPLEETECTIQGGEGYRGTVNTIWMGIPQQRWDSQYPHE 331
QY 301 HDMPTEPNFKDILRENYCNRPDSESSEWCTTTPNIRVGCSCQIPNCDSHSGDDCYRNG 360
DB 332 HDMPTEPNFKDILRENYCNRPDSESSEWCTTTPNIRVGCSCQIPNCDSHSGDDCYRNG 391
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QY 361 KNYMGNLSQTRSGLTCSMWDKXNMDLHRHIFWEPDASKLNENYCNRPDDAHGPMCTYGN 420
DB 392 KNYMGNLSQTRSGLTCSMWDKXNMDLHRHIFWEPDASKLNENYCNRPDDAHGPMCTYGN 451
QY 421 PLIPWDYCPISRCBGDTTPTIV 442
DB 452 PLIPWDYCPISRCBGDTTPTIV 473

RESULT 5
US-08-290-937B-1
Sequence 1, Application US/08290937B
Patent No. 5648233
GENERAL INFORMATION:
APPLICANT: YAMAGUCHI, KYOJI
APPLICANT: SHIMA, NOBUYUKI
APPLICANT: MURAKAMI, AKIHICO
APPLICANT: GOTO, MASAOKI
APPLICANT: TSUDA, EISUKE
APPLICANT: MASUNAGA, HIROAKI
APPLICANT: TAKAHIRA, REIKO
APPLICANT: OOGAKI, FUMIKO
APPLICANT: UEDA, MASATSUGU
APPLICANT: HIGASHIO, KANUJI
TITLE OF INVENTION: MODIFIED TCF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,937B
FILING DATE: 19-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-290-937B-1

Query Match      99.9%; Score 2576; DB 1; Length 723;
Best Local Similarity 99.8%; Pred. No. 1.9e-213;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRRTIHEFKSAKTTLLIKIDPALKITKRVNTADOCANRCTRNKGLPFTCKAFVFPK 60
DB 32 QRRKRTIHEFKSAKTTLLIKIDPALKITKRVNTADOCANRCTRNKGLPFTCKAFVFPK 91
QY 61 ARKQCLMPFPNSMSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKCOP 120
DB 92 ARKQCLMPFPNSMSSGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVSITKSGIKCOP 151
QY 121 WSSMIPIHEHSYRKDIOENYCNRPGBEGGPMCFTSNPEVRYEVCDIPOCSEVECTCNG 180
```

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Db 152 WSSMIPHEHSYRGKDLQENYCNPRGEGGPMCFITSNPEVRYEVCDDIPQCEVECMTCNG 211
Qy 181 ESYRGLMDHTSGKICQRMWDHOTPHRHKFLPERYPDKGFDNYCNRNPDGQPRMPCYTLDP 240
Db 212 ESYRGLMDHTSGKICQRMWDHOTPHRHKFLPERYPDKGFDNYCNRNPDGQPRMPCYTLDP 271
Qy 241 HTRWEYCAIKTCADNTMNDTVPLETTETCIGQGEGRGTNTIWMGIPQGRMDSQYPHE 300
Db 272 HTRWEYCAIKTCADNTMNDTVPLETTETCIGQGEGRGTNTIWMGIPQGRMDSQYPHE 331
Qy 301 HMTPEENFKCKDLRENYCNRNPDGSESPMCFITTDNIRVGYCSQIPNCDMSHGQDCYRNG 360
Db 332 HMTPEENFKCKDLRENYCNRNPDGSESPMCFITTDNIRVGYCSQIPNCDMSHGQDCYRNG 391
Qy 361 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNNYCNRPDDAHGPMCTYGN 420
Db 392 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNNYCNRPDDAHGPMCTYGN 451
Qy 421 PLIPWDYCPISRCEGDTTPTIV 442
Db 452 PLIPWDYCPISRCEGDTTPTIV 473
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## RESULT 6

```
US-08-290-937B-2
; Sequence 2, Application US/08290937B
; Patent No. 5648233
```

```
GENERAL INFORMATION:
APPLICANT: YAMAGUCHI, KYOJI
APPLICANT: SHIMA, NOBUYUKI
APPLICANT: MORAKAMI, AKIHICO
APPLICANT: GOTO, MASAKI
APPLICANT: TSUDA, EISUKE
APPLICANT: MASUNAGA, HIROAKI
APPLICANT: TAKAHIRA, REIKO
APPLICANT: OOGAKI, FUMIKO
APPLICANT: UEDA, MASATSUGU
APPLICANT: HIGASHIO, KANUJI
TITLE OF INVENTION: MODIFIED TCF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,937B
FILING DATE: 19-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION/DOCKET NUMBER: 32,503
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-290-937B-2
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Query Match

99.9%; Score 2576; DB 1; Length 723;

Best Local Similarity 99.8%; Pred. No. 1,9e-213;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ERKRNTHFEKSKAKTLLIKIDPALKIKTKXVNTADOCANRCRNKGLPFTCAFAVDK 60
Db 32 QKRNTHFEKSKAKTLLIKIDPALKIKTKXVNTADOCANRCRNKGLPFTCAFAVDK 91
Qy 61 ARKOLMFPFNSMSGVKEFGHEFDLYENKDYIRNCIIGKRSYKGVSTTKSGIKQP 120
Db 92 ARKOLMFPFNSMSGVKEFGHEFDLYENKDYIRNCIIGKRSYKGVSTTKSGIKQP 151
Qy 121 WSSMIPHEHSYRGKDLQENYCNPRGEGGPMCFITTDNIRVGYCSQIPNCDMSHGQDCYRNG 180
Db 152 WSSMIPHEHSYRGKDLQENYCNPRGEGGPMCFITSNPEVRYEVCDDIPQCEVECMTCNG 211
Qy 181 ESYRGLMDHTSGKICQRMWDHOTPHRHKFLPERYPDKGFDNYCNRNPDGQPRMPCYTLDP 240
Db 212 ESYRGLMDHTSGKICQRMWDHOTPHRHKFLPERYPDKGFDNYCNRNPDGQPRMPCYTLDP 271
Qy 241 HTRWEYCAIKTCADNTMNDTVPLETTETCIGQGEGRGTNTIWMGIPQGRMDSQYPHE 300
Db 272 HTRWEYCAIKTCADNTMNDTVPLETTETCIGQGEGRGTNTIWMGIPQGRMDSQYPHE 331
Qy 301 HMTPEENFKCKDLRENYCNRNPDGSESPMCFITTDNIRVGYCSQIPNCDMSHGQDCYRNG 360
Db 332 HMTPEENFKCKDLRENYCNRNPDGSESPMCFITTDNIRVGYCSQIPNCDMSHGQDCYRNG 391
Qy 361 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNNYCNRPDDAHGPMCTYGN 420
Db 392 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNNYCNRPDDAHGPMCTYGN 451
Qy 421 PLIPWDYCPISRCEGDTTPTIV 442
Db 452 PLIPWDYCPISRCEGDTTPTIV 473
```

## RESULT 7

```
US-08-404-643-1
; Sequence 1, Application US/08404643
; Patent No. 5658742
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```
GENERAL INFORMATION:
APPLICANT: HIGASHIO, KANUJI
APPLICANT: SHIMA, NOBUYUKI
APPLICANT: OOGAKI, FUMIKO
TITLE OF INVENTION: MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & THIBAUT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,643
FILING DATE: 15-MAR-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION/DOCKET NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-034 (3999/35)
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
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;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-404-643-1

```

Query Match	99.9%	Score 2576;	DB 1;	length 723;
Best Local Similarity	99.8%	Pred. No. 1.9e-213;		
Matches 441; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	:	ERRKRRNTIHEFKKSATYTLIKIDIPALKIKTKKVNADOCARCTRNGKLPTTCAAFYEDK	60
Dd	32	QRRGRNTIHEFKKSATYTLIKIDIPALKIKTKKVNADOCARCTRNGKLPTTCAAFYDK	91
Qy	61	ARRQCLMPFPNPNSSSGVCKKEFGHEFDLYENKDYINCCIIGGRSRYKTWSITTSKGIKOP	120
Dd	92	ARRQCLMPFPNPNSSSGVCKKEFGHEFDLYENKDYINCCIIGGRSRYKTWSITTSKGIKOP	151
Qy	121	WSMIMIHSHSYRKDLOENYCNRPGESEGPMPCFSPNSNEVRYEYCDIPQSEYVCMTCNG	180
Dd	152	WSMIMIHSHSYRKDLOENYCNRPGESEGPMPCFSPNSNEVRYEYCDIPQSEYVCMTCNG	211
Qy	181	ESYRGLMDHTESESKICQRMHDHOTPHNHKFLPERYPDKDFDNVYCNPNQDQRPMPCTYLPD	240
Dd	212	ESYRGLMDHTESESKICQRMHDHOTPHNHKFLPERYPDKDFDNVYCNPNQDQRPMPCTYLPD	271
Qy	241	HTREWYCAIKTCADNTMNDTVPLETTETCICQSGSGYRGYVNTIWNIGPCQRMDSQYPHE	300
Dd	272	HTREWYCAIKTCADNTMNDTVPLETTETCICQSGSGYRGYVNTIWNIGPCQRMDSQYPHE	331
Qy	301	HDHTPNPFCCKDLRENYCNRPNQSGSPMCFITDPDIRRGYCSQIPNCMSHGGDCYVNGG	360
Dd	332	HDHTPNPFCCKDLRENYCNRPNQSGSPMCFITDPDIRRGYCSQIPNCMSHGGDCYVNGG	391
Qy	361	KNYMGNLSQTRSGLTCSMMDKMMEDLHRIIFWEPDASKLLENYCNPNPDADHAGWCYTGK	420
Dd	392	KNYMGNLSQTRSGLTCSMMDKMMEDLHRIIFWEPDASKLLENYCNPNPDADHAGWCYTGK	451
Qy	421	PLIPMDYCPISRCBGJTTPTIIV	442
Dd	452	PLIPMDYCPISRCBGJTTPTIIV	473

RESULT 8  
US-09-194-326-1  
; Sequence 1, Application US/09194326

Query Match 99.9%; Score 2576; DB 3; Length 723;

Best Local Similarity 99.8%; Pred. No. 1,9e-213;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Qy	ERRKRATHEPKFSASATTLIKIDPLAKIKTKKVNADQCARCTRNGLPETPKAFYDK	60
Db	32 QRRKRATHEPKFSANATTLIKIDPLAKIKTKKVNADQCARCTRNGLPETPKAFYDK	91
Qy	61 ARKQCLMPFPNWSGSGVKKFEGHEFDLYENKDYINCLIGKRSYKGTSTITSKGIKOP	120
Db	92 ARKQCLMPFPNWSGSGVKKFEGHEFDLYENKDYINCLIGKRSYKGTSTITSKGIKOP	151
Qy	121 WSMIMIHHSYRQKDLQENYCNRPGEBSGPMCFNSBNRYEYVCDIPQSENVCMTCNG	180
Db	152 WSMIMIHHSYRQKDLQENYCNRPGEBSGPMCFNSBNRYEYVCDIPQSENVCMTCNG	211
Qy	181 ESYRGLMDHTESGKICQRWDHOTPRHRKFLPERYBDKGFDDNYCRNPDGQRPMPCTYLDP	240
Db	212 ESYRGLMDHTESGKICQRWDHOTPRHRKFLPERYBDKGFDDNYCRNPDGQRPMPCTYLDP	271
Qy	241 HTRWEYCAIKTCADNTMDTDVPLETTECIOQOGEYRGVNTIWNIGPCORWDQYRHE	300
Db	272 HTRWEYCAIKTCADNTMDTDVPLETTECIOQOGEYRGVNTIWNIGPCORWDQYRHE	331
Qy	301 HMDTPENPKCKDLREYCNRPDGSSEPMCFITTDPIRIVGYCSOIPNCDMSHGDCYVNG	360
Db	332 HMDTPENPKCKDLREYCNRPDGSSEPMCFITTDPIRIVGYCSOIPNCDMSHGDCYVNG	391
Qy	361 KNYMGNLSOTRSGLTCSMWDKXMEJLHRIEMEPDASKLNEYCNRPDDAHGWCYTCGN	420
Db	392 KNYMGNLSOTRSGLTCSMWDKXMEJLHRIEMEPDASKLNEYCNRPDDAHGWCYTCGN	451
Qy	421 PLIPMDYCPISRCBGDTPTIIV	442
Db	452 PLIPMDYCPISRCBGDTPTIIV	473

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RESULT 9
US-09-600-991-18
; Sequence 18, Application US/09600991
; Patent No. 6551991
; GENERAL INFORMATION:
; APPLICANT: MEDICO, Enzo
; APPLICANT: MICHELI, Paolo
; APPLICANT: COLLESI, Chiara
; APPLICANT: CASELLI, Gianfranco
; APPLICANT: CONOGLIO, Paolo
; TITLE OF INVENTION: RECOMBINANT PROTEINS DERIVED FROM HGF AND MSP
; FILE REFERENCE: 0471-0163P
; CURRENT APPLICATION NUMBER: US/09/600,991
; CURRENT FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-600-991-18

```

Query Match	99.9%	Score 2576;	DB 4;	length 723;
Best Local Similarity	99.8%	Pred. No. 1.9e-213;		
Matches 441; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0

QY ERKRRNTHEPKKSATTLTKIDPALTKTKKVVADQCARCRRNGLPPTCAFAFDK 60  
 Db QRRRRNTHEPKKSATTLTKIDPALTKTKKVVADQCARCRRNGLPPTCAFAFDK 91  
 QY ARQOCAMPFPPNMSSCVKKRGEHEDLYENDDYRNCIIGRGRYKTVSITSGIKCP 120  
 Db ARQOCAMPFPPNMSSCVKKRGEHEDLYENDDYRNCIIGRGRYKTVSITSGIKCP 151  
 QY WSSMIIDHEHSYRGKDLQENYCRNPGBEGGFWCFTSNBEVAYEVDI.PQCSVEVCMTCNG 180  
 Db WSSMIIDHEHSYRGKDLQENYCRNPGBEGGFWCFTSNBEVAYEVDI.PQCSVEVCMTCNG 211

QY 181 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDDNYCNRNPDGQPRPWCYTLD 240  
DB 212 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDDNYCNRNPDGQPRPWCYTLD 271  
QY 241 HTRMEYCAIKTCADNTMNDTVPLETTETCIGQGEYRGVTNTIWNIGIPQQRWDSQYPHE 300  
DB 272 HTRMEYCAIKTCADNTMNDTVPLETTETCIGQGEYRGVTNTIWNIGIPQQRWDSQYPHE 331  
QY 301 HDMTPENFKCDLRENYCNRNPDGSSPWCFTTDPNIRVGYCSQIIPNCMSHGQDCYRNG 360  
DB 332 HDMTPENFKCDLRENYCNRNPDGSSPWCFTTDPNIRVGYCSQIIPNCMSHGQDCYRNG 391  
QY 361 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 451  
QY 421 PLIPWDYCPISRCBGDTTPTIV 442  
DB 452 PLIPWDYCPISRCBGDTTPTIV 473

RESULT 10  
US-08-605-221-4  
; Sequence 4, Application US/08605221  
; Patent No. 669837  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, Toshikazu  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE  
; FILE REFERENCE: 2520-0101P  
; CURRENT APPLICATION NUMBER: US/08/605,221  
; CURRENT FILING DATE: 1996-03-15  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: HGF-B (five amino acids deletion type)  
US-08-605-221-4

Query Match 99.9%; Score 2576; DB 4; Length 723;  
Best Local Similarity 99.8%; Pred. No. 1.9e-213;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKRKRNTHEFKSAKTTLLIKIDPAIKTKKVNTPADQCANRCTRNKGLPTCKAFVFDK 60  
DB 32 QRRKNTHEFKSAKTTLLIKIDPAIKTKKVNTPADQCANRCTRNKGLPTCKAFVFDK 91  
QY 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKQCP 120  
DB 92 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKQCP 151  
QY 121 WSSMTPHEHSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCEVEECMTNG 180  
DB 152 WSSMTPHEHSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCEVEECMTNG 211  
QY 181 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDDNYCNRNPDGQPRPWCYTLD 240  
DB 212 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDDNYCNRNPDGQPRPWCYTLD 271  
QY 241 HTRMEYCAIKTCADNTMNDTVPLETTETCIGQGEYRGVTNTIWNIGIPQQRWDSQYPHE 300  
DB 272 HTRMEYCAIKTCADNTMNDTVPLETTETCIGQGEYRGVTNTIWNIGIPQQRWDSQYPHE 331  
QY 301 HDMTPENFKCDLRENYCNRNPDGSSPWCFTTDPNIRVGYCSQIIPNCMSHGQDCYRNG 360  
DB 332 HDMTPENFKCDLRENYCNRNPDGSSPWCFTTDPNIRVGYCSQIIPNCMSHGQDCYRNG 391  
QY 361 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 451

QY 421 PLIPWDYCPISRCBGDTTPTIV 442  
DB 452 PLIPWDYCPISRCBGDTTPTIV 473

RESULT 11  
US-09-601-040A-10  
; Sequence 10, Application US/09601040A  
; Patent No. 6730657  
; GENERAL INFORMATION:  
; APPLICANT: MEDICO, Enzo et al.  
; TITLE OF INVENTION: Recombinant Proteins from HGF and MSP  
; FILE REFERENCE: 0471-0161P  
; CURRENT APPLICATION NUMBER: US/09/601,040A  
; CURRENT FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-601-040A-10

Query Match 99.9%; Score 2576; DB 4; Length 723;  
Best Local Similarity 99.8%; Pred. No. 1.9e-213;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKRKRNTHEFKSAKTTLLIKIDPAIKTKKVNTPADQCANRCTRNKGLPTCKAFVFDK 60  
DB 32 QRRKNTHEFKSAKTTLLIKIDPAIKTKKVNTPADQCANRCTRNKGLPTCKAFVFDK 91  
QY 61 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKQCP 120  
DB 92 ARKQCLMPFPNMSGGVKKEFGHEFDLYENKDYIRNCIIIGKRSYKGTVISITKSGIKQCP 151  
QY 121 WSSMTPHEHSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCEVEECMTNG 180  
DB 152 WSSMTPHEHSYRGKDLQENYCRNPRGEGGFWCTSNPEVRYEVCDDIPQCEVEECMTNG 211  
QY 181 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDDNYCNRNPDGQPRPWCYTLD 240  
DB 212 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDDNYCNRNPDGQPRPWCYTLD 271  
QY 241 HTRMEYCAIKTCADNTMNDTVPLETTETCIGQGEYRGVTNTIWNIGIPQQRWDSQYPHE 300  
DB 272 HTRMEYCAIKTCADNTMNDTVPLETTETCIGQGEYRGVTNTIWNIGIPQQRWDSQYPHE 331  
QY 301 HDMTPENFKCDLRENYCNRNPDGSSPWCFTTDPNIRVGYCSQIIPNCMSHGQDCYRNG 360  
DB 332 HDMTPENFKCDLRENYCNRNPDGSSPWCFTTDPNIRVGYCSQIIPNCMSHGQDCYRNG 391  
QY 361 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMWDKXMDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTGN 451  
QY 421 PLIPWDYCPISRCBGDTTPTIV 442  
DB 452 PLIPWDYCPISRCBGDTTPTIV 473

RESULT 12  
US-09-601-040A-2  
; Sequence 2, Application US/09601040A  
; Patent No. 6730657  
; GENERAL INFORMATION:  
; APPLICANT: MEDICO, Enzo et al.  
; TITLE OF INVENTION: Recombinant Proteins from HGF and MSP  
; FILE REFERENCE: 0471-0161P  
; CURRENT APPLICATION NUMBER: US/09/601,040A  
; CURRENT FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2

LENGTH: 729  
TYPE: PR  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Recombinant sequence derived from Homo sapiens  
US-09-601-040A-2

Query Match 99.9%; Score 2576; DB 4; Length 729;  
Best Local Similarity 99.8%; Pred. No. 1.9e-213;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRRNTIHEPKSATTTLIKIDPALKIKTKKNTADQCANRCTRNGGLPFTCKARVFDK 60  
DB 32 ORKRRNTIHEPKSATTTLIKIDPALKIKTKKNTADQCANRCTRNGGLPFTCKARVFDK 91  
QY 61 ARKQCLMPFPNSSSGVKKEFGHEFDLYENKDIIRNCIIIGKRSYKGTVSITKSGIKCOP 120  
DB 92 ARKQCLMPFPNSSSGVKKEFGHEFDLYENKDIIRNCIIIGKRSYKGTVSITKSGIKCOP 151  
QY 121 WSSMIPHEHSYRGKDLOENYCRNPRGEGGPMCFSTNPEVRYEVCIPQSEVECMTCNG 180  
DB 152 WSSMIPHEHSYRGKDLOENYCRNPRGEGGPMCFSTNPEVRYEVCIPQSEVECMTCNG 211  
QY 181 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDNNYCRNPDGAPRWCYTLP 240  
DB 212 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDNNYCRNPDGAPRWCYTLP 271  
QY 241 HTRWEYCAIKTCADNTMNDTVPLETTETCIQGGEGYRGTVNTIWMGIPQQRWDSQYPHE 300  
DB 272 HTRWEYCAIKTCADNTMNDTVPLETTETCIQGGEGYRGTVNTIWMGIPQQRWDSQYPHE 331  
QY 301 HDMTPEPFCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGDDCYRGNG 360  
DB 332 HDMTPEPFCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGDDCYRGNG 391  
QY 361 KNYMGLSOTRSGLTCSMDKNMEDLHRHIFWEPPDASKLNENYCRNPDGAPRWCYTGN 420  
DB 392 KNYMGLSOTRSGLTCSMDKNMEDLHRHIFWEPPDASKLNENYCRNPDGAPRWCYTGN 451  
QY 421 PLIPWDYCPISRCEGDTPTTIV 442  
DB 452 PLIPWDYCPISRCEGDTPTTIV 473

RESULT 13  
US-09-601-040A-4  
Sequence 4, Application US/09601040A  
Patent No. 6730657  
GENERAL INFORMATION:  
APPLICANT: MEDICO, Enzo et al.  
TITLE OF INVENTION: Recombinant Proteins from HGF and MSP  
FILE REFERENCE: 0471-0161P  
CURRENT APPLICATION NUMBER: US/09/601, 040A  
CURRENT FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 729  
TYPE: PR  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Recombinant sequence derived from Homo sapiens  
US-09-601-040A-4

Query Match 99.9%; Score 2576; DB 4; Length 729;  
Best Local Similarity 99.8%; Pred. No. 1.9e-213;  
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRRNTIHEPKSATTTLIKIDPALKIKTKKNTADQCANRCTRNGGLPFTCKARVFDK 60  
DB 32 ORKRRNTIHEPKSATTTLIKIDPALKIKTKKNTADQCANRCTRNGGLPFTCKARVFDK 91  
QY 61 ARKQCLMPFPNSSSGVKKEFGHEFDLYENKDIIRNCIIIGKRSYKGTVSITKSGIKCOP 120

DB 92 ARKQCLMPFPNSSSGVKKEFGHEFDLYENKDIIRNCIIIGKRSYKGTVSITKSGIKCOP 151  
QY 121 WSSMIPHEHSYRGKDLOENYCRNPRGEGGPMCFSTNPEVRYEVCIPQSEVECMTCNG 180  
DB 152 WSSMIPHEHSYRGKDLOENYCRNPRGEGGPMCFSTNPEVRYEVCIPQSEVECMTCNG 211  
QY 181 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDNNYCRNPDGAPRWCYTLP 240  
DB 212 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDNNYCRNPDGAPRWCYTLP 271  
QY 241 HTRWEYCAIKTCADNTMNDTVPLETTETCIQGGEGYRGTVNTIWMGIPQQRWDSQYPHE 300  
DB 272 HTRWEYCAIKTCADNTMNDTVPLETTETCIQGGEGYRGTVNTIWMGIPQQRWDSQYPHE 331  
QY 301 HDMTPEPFCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGDDCYRGNG 360  
DB 332 HDMTPEPFCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDSHGDDCYRGNG 391  
QY 361 KNYMGLSOTRSGLTCSMDKNMEDLHRHIFWEPPDASKLNENYCRNPDGAPRWCYTGN 420  
DB 392 KNYMGLSOTRSGLTCSMDKNMEDLHRHIFWEPPDASKLNENYCRNPDGAPRWCYTGN 451  
QY 421 PLIPWDYCPISRCEGDTPTTIV 442  
DB 452 PLIPWDYCPISRCEGDTPTTIV 473

RESULT 14  
US-08-030-410-3  
Sequence 3, Application US/08030410  
Patent No. 6221359  
GENERAL INFORMATION:  
APPLICANT: Komiya, Atsushi  
APPLICANT: Nakahata, Tatsutoshi  
APPLICANT: Kudo, Tetsuo  
APPLICANT: Tanaka, Ryunhei  
APPLICANT: Kawano, Genji  
APPLICANT: Sudo, Tetsuo  
APPLICANT: Sano, Emiko  
APPLICANT: Kojima, Katsunaki  
TITLE OF INVENTION: HEMOPOIETIC STEM CELL MULTIPLIER  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,410  
FILING DATE: 19930521  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Digilio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 8898  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-030-410-3

Query Match 99.8%; Score 2573; DB 3; Length 723;  
Best Local Similarity 99.5%; Pred. No. 3 4e-213;  
Matches 440; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERKRNTTHERFKSAKTTLIKIDPALKITKTKVNTADOCANRCTRNKGLPFTCKAFVFDK 60  
DB 32 ORKRNTTHERFKSAKTTLIKIDPALKITKTKVNTADOCANRCTRNKGLPFTCKAFVFDK 91  
QY 61 ARKQCLMPFNSMSGVKKERFHEFDLYENKDYIRNCIIIGKRSYKGVSTIKSGIKOP 120  
DB 92 ARKQCLMPFNSMSGVKKERFHEFDLYENKDYIRNCIIIGKRSYKGVSTIKSGIKOP 151  
QY 121 WSSMTPHESYRGKDLQENYCRNPRGEGGPMCFSTNPEVREYVCDIPQCSVEECMTGNG 180  
DB 152 WSSMTPHESYRGKDLQENYCRNPRGEGGPMCFSTNPEVREYVCDIPQCSVEECMTGNG 211  
QY 161 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLDP 240  
DB 212 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLDP 271  
QY 241 HTRMEYCAIKTCADNTMNDTVPLETTTCIOGGGSGYGTNTIWNGLPCQRMDSQYPHE 300  
DB 272 HTRMEYCAIKTCADNTMNDTVPLETTTCIOGGGSGYGTNTIWNGLPCQRMDSQYPHE 331  
QY 301 HDMTEPNFKCDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGOQDCYRGNG 360  
DB 332 HDMTEPNFKCDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGOQDCYRGNG 391  
QY 361 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNNYCRNPDGDAHGPWCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNNYCRNPDGDAHGPWCYTGN 451  
QY 421 PLIPWDYCPISRCEGDTPTIV 442  
DB 452 PLIPWDYCPISRCEGDTPTIV 473

RESULT 15

US-08-290-937B-3

; Sequence 3, Application US/08230937B

; Patent No. 5648233

; GENERAL INFORMATION:

; APPLICANT: YAMAGUCHI, KYOJI

; APPLICANT: SHIMA, NOBUYUKI

; APPLICANT: MURAKAMI, AKIHICO

; APPLICANT: GOTO, MASAAKI

; APPLICANT: TSUDA, EISUKE

; APPLICANT: MASUNAGA, HIROAKI

; APPLICANT: TAKAHIRA, REIKO

; APPLICANT: OOGAKI, FUMIKO

; APPLICANT: UEDA, MASATSUGU

; APPLICANT: HIGASHIO, KANJI

; TITLE OF INVENTION: MODIFIED TCF

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Testa, Hurwitz &amp; Thibault

; STREET: 125 High St.

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/290,937B

; FILING DATE: 19-AUG-1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

;

;

;

;

;

;

NAME: CAMPBELL, PAULA A.

REGISTRATION NUMBER: 32,503

REFERENCE/DOCKET NUMBER: FJN-022

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 723 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-290-937B-3

Query Match 99.7%; Score 2570; DB 1; Length 723;  
Best Local Similarity 99.5%; Pred. No. 6 1e-213;  
Matches 440; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ERKRNTTHERFKSAKTTLIKIDPALKITKTKVNTADOCANRCTRNKGLPFTCKAFVFDK 60  
DB 32 ORKRNTTHERFKSAKTTLIKIDPALKITKTKVNTADOCANRCTRNKGLPFTCKAFVFDK 91  
QY 61 ARKQCLMPFNSMSGVKKERFHEFDLYENKDYIRNCIIIGKRSYKGVSTIKSGIKOP 120  
DB 92 ARKQCLMPFNSMSGVKKERFHEFDLYENKDYIRNCIIIGKRSYKGVSTIKSGIKOP 151  
QY 121 WSSMTPHESYRGKDLQENYCRNPRGEGGPMCFSTNPEVREYVCDIPQCSVEECMTGNG 180  
DB 152 WSSMTPHESYRGKDLQENYCRNPRGEGGPMCFSTNPEVREYVCDIPQCSVEECMTGNG 211  
QY 161 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLDP 240  
DB 212 ESYRGLMDHTESGKICQRMWDHQTPIRHKFLPERYPDKGFDNNYCRNPDGQPRPWCYTLDP 271  
QY 241 HTRMEYCAIKTCADNTMNDTVPLETTTCIOGGGSGYGTNTIWNGLPCQRMDSQYPHE 300  
DB 272 HTRMEYCAIKTCADNTMNDTVPLETTTCIOGGGSGYGTNTIWNGLPCQRMDSQYPHE 331  
QY 301 HDMTEPNFKCDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGOQDCYRGNG 360  
DB 332 HDMTEPNFKCDLRENYCRNPDGSESPMCFTTDPNIRVGYCSQIPNCDSHGOQDCYRGNG 391  
QY 361 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNNYCRNPDGDAHGPWCYTGN 420  
DB 392 KNYMGNLSQTRSGLTCSMWDKXMEDLHRHIFWEPDASKLNNYCRNPDGDAHGPWCYTGN 451  
QY 421 PLIPWDYCPISRCEGDTPTIV 442  
DB 452 PLIPWDYCPISRCEGDTPTIV 473

Search completed: October 3, 2005, 06:53:49  
Job time : 1361.31 secs